

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 25, 2004, 14:09:19 ; Search time 118 Seconds  
(without alignments)  
9.578 Million cell updates/sec

Title: US-10-053-669-2  
Perfect score: 21  
Sequence: 1 FGLM 4

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 15518

Minimum DB seq length: 0  
Maximum DB seq length: 4

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*

- 1: geneseqp1980s:\*
- 2: geneseqp1990s:\*
- 3: geneseqp2000s:\*
- 4: geneseqp2001s:\*
- 5: geneseqp2002s:\*
- 6: geneseqp2003as:\*
- 7: geneseqp2003bs:\*
- 8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	4	2 AAW41683	Aaw41683 Peptide u
2	21	100.0	4	2 AAY31075	Aay31075 Non-cross
3	21	100.0	4	3 AAB23026	Aab23026 Human/rat
4	21	100.0	4	3 AAY67577	Aay67577 P antagonist
5	21	100.0	4	4 AAB91447	Aab91447 Tachykini
6	21	100.0	4	5 ABB10091	Abb10091 Substance
7	21	100.0	4	5 AAU77846	Aau77846 Tachykini
8	18	85.7	4	1 AAP61654	Aap61654 Sequence
9	18	85.7	4	1 AAP71301	Aap71301 Peptide c
10	18	85.7	4	2 AAW41686	Aaw41686 Tetrapept
11	18	85.7	4	5 ABB10092	Abb10092 Substance
12	16	76.2	4	1 AAP61707	Aap61707 Sequence
13	16	76.2	4	1 AAP71312	Aap71312 Peptide c
14	16	76.2	4	2 AAY23485	Aay23485 V beta 6
15	16	76.2	4	3 AAB12293	Aab12293 Prodrug o
16	16	76.2	4	4 AAG62647	Aag62647 Typical t
17	16	76.2	4	5 ABB88046	Abb88046 Enzyme cl
18	15	71.4	3	3 AAY67578	Aay67578 P antagonist
19	15	71.4	4	4 AAB91448	Aab91448 Tachykini
20	15	71.4	4	1 AAP60334	Aap60334 Peptide w
21	15	71.4	4	2 AAW77469	Aaw77469 Tetrapept
22	15	71.4	4	2 AAW41684	Aaw41684 Tetrapept
23	15	71.4	4	2 AAW41685	Aaw41685 Tetrapept
24	15	71.4	4	4 AAB91795	Aab91795 Amyloid b
25	15	71.4	4	4 AAB91822	Aab91822 Amyloid b

26	14	66.7	4	1 AAP61659	Aap61659 Sequence
27	14	66.7	4	1 AAP71306	Aap71306 Peptide c
28	14	66.7	4	2 AAR34486	Aar34486 FGIA. 8/1
29	14	66.7	4	2 AAR46020	Aar46020 Serine pr
30	14	66.7	4	2 AAR93149	Aar93149 Mycobacte
31	14	66.7	4	3 AAB12292	Aab12292 Prodrug o
32	14	66.7	4	4 AAB91714	Aab91714 Opioid pe
33	14	66.7	4	5 ABB88045	Abb88045 Enzyme cl
34	14	66.7	4	5 ABG32223	Abg32223 Sheep col
35	13	61.9	3	5 ABG77484	Abg77484 Targettin
36	13	61.9	4	1 AAP61658	Aap61658 Sequence
37	13	61.9	4	1 AAP71287	Aap71287 Opiate bi
38	13	61.9	4	1 AAR82591	Aar82591 Renin inh
39	13	61.9	4	2 AAR15768	Aar15768 Farnesyl-
40	13	61.9	4	2 AAR47299	Aar47299 Peptide a
41	13	61.9	4	2 AAR47301	Aar47301 Peptide a
42	13	61.9	4	2 AAR49765	Aar49765 Farnesyl
43	13	61.9	4	2 AAR77829	Aar77829 Farnesyl
44	13	61.9	4	2 AAR84314	Aar84314 Human/Bov
45	13	61.9	4	2 AAW04455	Aaw04455 Farnesyl

ALIGNMENTS

RESULT 1  
AAW41683  
ID AAW41683 standard; peptide; 4 AA.  
XX  
AC AAW41683;  
XX  
DT 09-JUN-1998 (first entry)  
XX  
DE Peptide used in ophthalmic drug to treat corneal disorders.  
XX  
KW Ophthalmic drug; corneal disorder; ulcer; epithelial peeling; dry eye;  
KW keratitis; insulin like growth factor-I; IGF-I; eye drop.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 4 /note= "C-terminal amide"  
XX  
FN WO9749419-A1.  
XX  
PD 31-DEC-1997.  
XX  
PF 11-JUN-1997; 97WO-JP002015.  
XX  
PR 26-JUN-1996; 96JP-00165612.  
XX  
PA (SANT ) SANTEN PHARM CO LTD.  
XX  
PI Nishida T, Nakamura M, Nakata K;  
XX  
DR WPI; 1998-076907/07.  
XX  
PT Ophthalmic drug composition containing tetra:peptide - is useful as  
PT corneal disorder remedy for corneal ulcer, corneal epithelial peeling,  
PT dry eye, keratitis.  
XX  
PS Claim 1; Page 15; 19pp; Japanese.  
XX  
CC The present sequence represents a tetrapeptide which is the active  
CC ingredient in an ophthalmic drug composition. It is used together with  
CC insulin like growth factor-I (IGF-I), to treat corneal disorders such as  
CC corneal ulcer, corneal epithelial peeling, dry eye and keratitis. The  
CC dosage is 0.1-5000 (preferably 1-1000) mg/day of the tetrapeptide and  
CC 0.001-100 (preferably 0.01-10) mg/day of IGF-I. The preferable form of  
CC the composition is eye drops  
XX  
SQ Sequence 4 AA;

Query Match 100.0%; Score 21; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4  
 ||||  
 Db 1 FGLM 4

RESULT 2  
 AAY31075  
 ID AAY31075 standard; peptide; 4 AA.  
 XX  
 AC AAY31075;  
 XX  
 DT 21-OCT-1999 (first entry)  
 XX  
 DE Non-crosslinked protein particle peptide 124.  
 XX  
 KW Non-crosslinked protein particle; diagnostic; therapy; monodisperse;  
 KW albumin; haemoglobin; nanometer; micrometer; clearance.  
 XX  
 OS Synthetic.

Key Location/Qualifiers  
 Modified-site 4 /note= "C-terminal amide"  
 FT  
 FT

US5945033-A.

31-AUG-1999.

12-NOV-1996; 96US-00747137.

15-JAN-1991; 91US-00641720.

13-OCT-1992; 92US-00959560.

01-JUN-1993; 93US-00069831.

14-MAR-1994; 94US-00212546.

(HEMO-) HEMOSPHERE INC.

Yen RCK;

WPI; 1999-508153/42.

Non-crosslinked protein particles for therapeutic and diagnostic use.

Example 22; Col 103-104; 65pp; English.

This invention describes a novel aqueous suspension of monodisperse particles on non-crosslinked, non-denatured albumin (50-5000 nm) which is stable against dissolving upon dilution with an alcohol-free aqueous medium. The method involves (a) forming an aqueous solution containing albumin and hemoglobin and (b) treating the aqueous solution with an alcohol to cause the solution to become turbid. The particles are useful as agents for in vivo administration, either of their own administration or as a vehicle for other therapeutic or diagnostic agents. The method permits the formation of albumin and hemoglobin particles in the nanometer and micrometer size range, in a form closer to their natural form than the forms of the prior art. The particles therefore constitute a more closely controlled agent for in vivo administration, with greater ease of clearance from the body after their period of usefulness. CC AAY30952-Y31135 represent peptides used in the method of the invention

Sequence 4 AA;

Query Match 100.0%; Score 21; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4  
 ||||

Db 1 FGLM 4

RESULT 3  
 AAB23026  
 ID AAB23026 standard; peptide; 4 AA.

XX

AC AAB23026;

XX

DT 16-JAN-2001 (first entry)

XX

Human/rat tachykinin Substance P C-terminal tetrapeptide.

Substance P; tachykinin; human; rat; magnesium binding defect;

sodium sensitive essential hypertension; insulin resistance;

type 2 diabetes; antibody; immunoassay; quantification.

XX

OS Homo sapiens.

OS Rattus sp.

XX

XX

Key Location/Qualifiers

Modified-site 4 /note= "C-terminal amide"

FT

FT

XX

XX

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XX

XX

XX

XX

XX

AC AAY67577;  
 XX  
 DT 19-MAY-2000 (first entry)  
 XX  
 DE P antagonist peptide #5.  
 XX  
 XX Pharmaceutical; veterinary; gonadotropin-releasing hormone; GnRH;  
 KW pore-forming agent; lecithin; stearin; P antagonist.  
 XX  
 XX Unidentified.  
 XX  
 XX Key Location/Qualifiers  
 FT Modified-site 4  
 FT /note= "C-terminal amide"  
 XX  
 PN WO200004897-A1.  
 XX  
 PD 03-FEB-2000.  
 XX  
 XX 20-JUL-1999; 99WO-AU000585.  
 XX  
 PR 20-JUL-1998; 98AU-00004730.  
 PR 20-JUL-1998; 98AU-00004731.  
 PR 13-MAY-1999; 99AU-00000324.  
 XX  
 XX (PEPT-) PEPTTECH LTD.  
 XX  
 PI Trigg TE, Walsh JD, Rathjen DA;  
 DR WPI; 2000-182528/16.  
 XX  
 PT Bioimplant formulation for sustained delivery of an active agent over 7  
 PT days to 2 years, comprises active agent, pore-forming agent and stearin.  
 XX  
 PS Claim 20; Page 21; 37pp; English.  
 XX  
 CC The invention provides a pharmaceutical and/or veterinary formulation  
 CC that comprises 2 - 30% of active agents which include a gonadotropin-  
 CC releasing hormone (GnRH) agonist, 0.5 - 20% of a pore-forming agent which  
 CC is not lecithin, and the remainder stearin. The formulation is useful as  
 CC a sustained release implant which can deliver the active agent for a  
 CC period of 7 days to 2 years. Sequences AAY67573-578 represent P  
 CC antagonist peptides used in the composition  
 XX  
 SQ Sequence 4 AA;  
 Query Match 100.0%; Score 21; DB 3; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FGLM 4  
 DB 1 FGLM 4  
 RESULT 5  
 ID AAB91447  
 XX AAB91447 standard; peptide; 4 AA.  
 AC AAB91447;  
 XX  
 DT 22-JUN-2001 (first entry)  
 XX  
 DE Tachykinins peptide SEQ ID NO:623.  
 XX  
 KW Protection; endogenous therapeutic peptide; peptidase; conjugation;  
 KW blood component; modification; succinimide; maleimide group; amino;  
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO200069900-A2.

XX 23-NOV-2000.  
 PD  
 XX 17-MAY-2000; 2000WO-US013576.  
 PF  
 XX 17-MAY-1999; 99US-0134406P.  
 PR 10-SEP-1999; 99US-0153406P.  
 PR 15-OCT-1999; 99US-0159783P.  
 XX  
 XX (CONJ-) CONJUCHEM INC.  
 XX  
 XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;  
 PI WPI; 2001-112059/12.  
 XX  
 DR Modifying and attaching therapeutic peptides to albumin prevents  
 PT peptidase degradation, useful for increasing length of in vivo activity.  
 PT  
 XX Disclosure; Page 402; 73pp; English.  
 PS  
 XX The present invention describes a modified therapeutic peptide (I)  
 CC comprising a therapeutically active amino acid region (III) and a  
 CC reactive group (II) (e.g. succinimide and maleimide groups) attached to  
 CC a less therapeutically active amino acid region (IV), which covalently  
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a  
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.  
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth  
 CC factors and neurotransmitters, to protect them from peptidase activity in  
 CC vivo for the treatment of various disorders. Endogenous therapeutic  
 CC peptides are not suitable as drug candidates as they require frequent  
 CC administration due to rapid degradation by peptidases in the body.  
 CC Modifying and attaching therapeutic peptides to albumin prevents or  
 CC reduces the action of peptidases to increase length of activity (half  
 CC life) and specificity as bonding to large molecules decreases  
 CC intracellular uptake and interference with physiological processes.  
 CC AAB90829 to AAB92441 represent peptides which can be used in the  
 CC exemplification of the present invention  
 XX  
 SQ Sequence 4 AA;  
 Query Match 100.0%; Score 21; DB 4; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FGLM 4  
 DB 1 FGLM 4  
 RESULT 6  
 ID ABB10091  
 XX ABB10091 standard; peptide; 4 AA.  
 AC ABB10091;  
 XX  
 XX 26-JUL-2002 (first entry)  
 DT  
 XX Substance P analog used in wound healing treatment#14.  
 DE  
 XX Wound healing; insulin-like growth factor-I; tear; abrasion; skin ulcer;  
 KW surgical incision; burn.  
 KW  
 XX Unidentified.  
 OS  
 XX WO200213853-A1.  
 PN  
 XX 21-FEB-2002.  
 PD  
 XX 10-AUG-2001; 2001WO-JP006933.  
 PF  
 XX 10-AUG-2000; 2000JP-00242489.  
 PR 28-NOV-2000; 2000JP-00361388.  
 XX

CC	This invention relates to novel therapeutic compounds and methods used
CC	for treating mammals with disorders such as salt-insensitive
CC	hypertension. The monopeptide compounds of the invention are derived from
CC	butadienes, ethylenes and propanes. The compounds of the invention are
CC	used to correct a defect in magnesium binding within the plasma membranes
CC	of somatic cells which results in a decrease in the intracellular
CC	concentration of magnesium ions. These compounds may be used in the
CC	treatment of a mammal affected with magnesium binding defect, salt-
CC	sensitive (particularly hypertension), insulin resistance of type 2
CC	diabetes mellitus and pre-eclampsia/eclampsia. The compounds of the
CC	invention have an advantage over prior art compounds in that these
CC	compounds are biologically stable. The present sequence represents the a
CC	tetrapeptide from the C terminal sequence of tachykinin known as
CC	substance P, this peptide is sufficient to correct the magnesium binding
CC	defect responsible for causing hypertension
XX	
SQ	Sequence 4 AA;
	Query Match 100.0%; Score 21; DB 5; Length 4;
	Best Local Similarity 100.0%; Pred. No. 1.4e+06;
	Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 FGLM 4
DB	1 FGLM 4
RESULT 8	
AAP61654	
ID	AAP61654 standard; peptide; 4 AA.
AC	AAP61654;
XX	
DT	25-MAR-2003 (revised)
DT	03-OCT-2002 (revised)
DT	21-AUG-1991 (first entry)
XX	
DE	Sequence of peptide which inhibits cyclic-nucleotide independent protein
DE	kinase activity and mammalian cell growth.
XX	
KW	Cell growth inhibitor; tumour cell growth inhibitor.
XX	
OS	Synthetic.
XX	
PH	Key Location/Qualifiers
FT	Misc-difference 1
FT	Misc-difference 4/label= Carbobenzoxy-Phe
FT	Misc-difference 4/label= Leu-CH2Cl
FT	
XX	
PN	US4582821-A.
XX	
PD	15-APR-1986.
XX	
PP	16-NOV-1983; 83US-00552255.
XX	
PR	16-NOV-1983; 83US-00552255.
XX	
PA	(DUPO ) DU PONT DE NEMOURS & CO E I.
XX	
PI	Kettner CA, Racker E;
DR	WPI; 1986-118872/18.
XX	
PT	Inhibition of tumour cell growth - using peptide and aminoacid
PT	halo:methyl ketone(s).
XX	
PS	Claim 1; Col 4; 9pp; English.
XX	
CC	The cpds. of the invention inhibit protein phosphorylation. The inventors
CC	claim a process for inhibiting the growth of tumour cells in a medium
CC	which comprises contacting the cells with a cpd. of formula (AAP61654-
CC	p61661) or a physiologically acceptable salt. (Updated on 03-OCT-2002 to



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CC add missing OS field.) (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 4 AA;

Query Match      85.7%; Score 18; DB 1; Length 4;
Best Local Similarity 75.0%; Pred. No. 1.4e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4
DB 1 FGLL 4

RESULT 9
AAP71301
ID AAP71301 standard; peptide; 4 AA.
XX
AC AAP71301;
XX
XX 25-MAR-2003 (revised)
DT 15-MAY-1991 (first entry)
XX
DE Peptide component of cpd. for treating picornavirus infections.
XX
XX Picornaviridae; poliovirus; rhinovirus; antiviral agent.
XX
XX Synthetic.
XX
XX US4636492-A.
XX
XX 13-JAN-1987.
XX
XX 29-AUG-1984; 84US-00645426.
XX
XX 29-AUG-1984; 84US-00645426.
XX
XX (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
XX Kettner CA, Korant BD;
XX
XX WPI; 1987-036897/05.
XX
XX Treating picorna-virus infection with peptide halo:methyl ketone cpds. -
PT esp. for treating polio virus and rhino virus infections.
XX
XX Disclosure; Page 3; 10pp; English.
XX
XX This peptide is useful as part of a peptide/halo-methyl ketone cpd., for
CC treating picornavirus, egpolio- or rhinovirus infections. It inhibits the
CC processing of picornavirus capsid proteins by virus encoded proteases.
CC See AAP71302-13. See also US4652552. (Updated on 25-MAR-2003 to correct
CC PA field.)
XX
SQ Sequence 4 AA;

Query Match      85.7%; Score 18; DB 1; Length 4;
Best Local Similarity 75.0%; Pred. No. 1.4e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4
DB 1 FGLL 4

RESULT 10
AAW41686
ID AAW41686 standard; peptide; 4 AA.
XX
XX AAW41686;
XX
XX 09-JUN-1998 (first entry)
DT
XX
DE Tetrapeptide #3.

XX
KW Ophthalmic drug; corneal disorder; ulcer; epithelial peeling; dry eye;
KW keratitis; insulin like growth factor-I; IGF-I; eye drop.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 4
FT /note= "C-terminal amide"

XX
XX WO9749419-A1.
XX
XX 31-DEC-1997.
XX
XX 11-JUN-1997; 97WO-JP002015.
XX
XX 26-JUN-1996; 96JP-00165612.
XX
XX (SANT ) SANTEN PHARM CO LTD.
XX
XX Nishida T, Nakamura M, Nakata K;
XX
XX WPI; 1998-076907/07.
XX
XX Ophthalmic drug composition containing tetra:peptide - is useful as
PT corneal disorder remedy for corneal ulcer, corneal epithelial peeling,
PT dry eye, keratitis.
XX
XX Disclosure; Page 11; 19pp; Japanese.
XX
XX This sequence is shown in the specification. The invention relates to an
CC ophthalmic drug composition which contains Phe-Gly-Leu-Met-NH2 or its
CC medicinally acceptable salts as the active ingredient. It is used,
CC together with insulin like growth factor-I (IGF-I), to treat corneal
CC disorders such as corneal ulcer, corneal epithelial peeling, dry eye and
CC keratitis. The dosage is 0.1-5000 (preferably 1-1000) mg/day of the
CC active ingredient and 0.001-100 (preferably 0.01-10) mg/day of IGF-I. The
CC preferable form of the composition is eye drops
XX
XX Sequence 4 AA;

Query Match      85.7%; Score 18; DB 2; Length 4;
Best Local Similarity 75.0%; Pred. No. 1.4e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4
DB 1 YGLM 4

RESULT 11
ABB10092
ID ABB10092 standard; peptide; 4 AA.
XX
XX ABB10092;
XX
XX 26-JUL-2002 (first entry)
DT
XX
DE Substance P analog used in wound healing treatment#15.
XX
XX Wound healing; insulin-like growth factor-I; tear; abrasion; skin ulcer;
KW surgical incision; burn.
XX
XX Unidentified.
XX
XX WO200213853-A1.
XX
XX 21-FEB-2002.
XX
XX 10-AUG-2001; 2001WO-JP006933.
XX
XX 10-AUG-2000; 2000JP-00242489.
XX
XX 28-NOV-2000; 2000JP-00361388.
PR

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RESULT 14
AAY23485
ID AAY23485 standard; peptide; 4 AA.
XX
AC AAY23485;
XX
DT 02-SEP-1999 (first entry)
XX
DE V beta 6 clone found in MS patients after vaccination with TCR.
XX
KW Vaccine; T cell receptor; TCR; T cell; V beta 6.2/3; V beta 6/5;
V beta 6.7; V beta 2; V beta 5/1; V beta 7; V beta 13; V beta 6;
KW multiple sclerosis.
XX
OS Synthetic.
OS Homo sapiens.
XX
FN WO9927957-A1.
XX
PD 10-JUN-1999.
XX
PF 03-DEC-1997; 97WO-US023147.
XX
PR 03-DEC-1997; 97WO-US023147.
XX
PA (IMMU-) IMMUNE RESPONSE CORP.
PA (KIMM-) KIMMEL CANCER CENT SIDNEY.
XX
PI Brostoff SW, Wilson DB, Smith LR, Gold DP, Carlo DJ;
XX
DR WPI; 1999-404801/34.
XX
PT T0 cell receptor peptide-derived vaccines.
XX
ES Example 11; Page 90; 104pp; English.
XX
CC The specification describes vaccines which comprise immunologically
effective amounts of T cell receptor (TCR) peptides. The TCRs are present
on the surface of T cells. The TCRs are chosen from V beta 6.2/3, V beta
6/5, V beta 6.7, V beta 2, V beta 5/1, V beta 7 or V beta 13. The V beta
TCR peptide-based vaccines are useful for prevention or treatment of
multiple sclerosis (MS). The presence of V beta 6.7 appears to be
particularly associated with multiple sclerosis and can be used to
determine an individual's susceptibility to multiple sclerosis.
CC Vaccinating, rather than passively administering heterologous antibodies,
allows the host's own immune system to mobilize and suppress auto
aggressive T cells. Therefore, the suppression is persistent and may
involve any and all immunological mechanisms in effecting that
suppression. Such a multi-faceted response is more effective than the uni
-dimensional suppression achieved by passive administration of monoclonal
antibodies or extant-derived regulatory T cell clones. AAY23481-Y23516
CC represent peptides derived from TCR V beta 6 clones found in the
CC cerebrospinal fluid (CSF) of MS patients, after vaccination with V beta 6
XX
SQ Sequence 4 AA;

Query Match 76.2%; Score 16; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGL 3
Db 1 FGL 3

RESULT 15
AAB12293
ID AAB12293 standard; peptide; 4 AA.
XX
AC AAB12293;
XX
DT 10-NOV-2000 (first entry)
XX

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DE Prodrug oligopeptide # 9.
XX
KW Prodrug; drug; antitumour; cancer; inflammation; rheumatic disease;
infection; breast; colorectal; liver; lung; prostate; ovarian; brain;
pancreatic; human; chemotherapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT /label= bala
FT /note= "beta-Alanine"
XX
FN WO200033888-A2.
XX
PD 15-JUN-2000.
XX
PF 10-DEC-1999; 99WO-US030393.
XX
PR 11-DEC-1998; 98US-0111793P.
PR 08-FEB-1999; 99US-0119312P.
XX
PA (COUS ) COULTER PHARM INC.
XX
PI Lobl TJ, Dubois V, Fernandez A, Gangwar S, Lewis E, Nieder MH;
PI Trouet A, Viski P, Yarranton GT;
XX
DR WPI; 2000-451793/39.
XX
PT Novel prodrug compound useful for treating cancer and inflammatory
diseases comprises a therapeutic agent capable of entering a target cell,
an oligopeptide, a stabilizer and optionally a linker.
XX
PS Claim 12; Page 53; 125pp; English.
XX
CC The present invention relates to a prodrug form of a therapeutic agent
linked to an oligopeptide, which in turn is linked to a stabilising
group. The present sequence is one such oligopeptide used in the present
invention. The prodrug may be used in chemotherapy for the treatment of
cancer such as that of breast, lung, prostate, ovary, brain or pancreas,
inflammatory disorders such as rheumatic diseases and infectious diseases
XX
SQ Sequence 4 AA;

Query Match 76.2%; Score 16; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGL 3
Db 2 FGL 4

Search completed: August 25, 2004, 14:22:16
Job time : 121 secs

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Blank sheet

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 25, 2004, 14:18:15 ; Search time 38 Seconds  
(without alignments)  
10.125 Million cell updates/sec

Title: US-10-053-669-2

Perfect score: 21

Sequence: 1 FGLM 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 86

Minimum DB seq length: 0  
Maximum DB seq length: 4

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PTR 78:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	DB	ID	Description
1	10	47.6	4	2	PT0240	Ig heavy chain CRD
2	10	47.6	4	2	A53284	T-cell receptor be
3	8	38.1	4	2	PT0633	T-cell receptor be
4	7	33.3	3	3	B23751	spinal cord peptid
5	7	33.3	4	2	E44823	synaptosomal-assoc
6	7	33.3	4	2	B53284	T-cell receptor be
7	6	28.6	3	3	GKHU	growth-modulating
8	6	28.6	3	3	A60898	bursin - chicken
9	6	28.6	3	3	A3751	spinal cord peptid
10	6	28.6	3	3	PT0636	T-cell receptor be
11	6	28.6	3	3	PT0571	T-cell receptor be
12	6	28.6	3	3	S68328	blood cell protein
13	6	28.6	4	1	EXAA	ancho-RFamide neur
14	6	28.6	4	2	A32039	tyrosine-melanocyt
15	6	28.6	4	2	ECNK	cardioexcitatory n
16	6	28.6	4	2	PL0140	carbon-monoxide de
17	6	28.6	4	2	D41654	hypothetical prote
18	6	28.6	4	2	S53508	starvation-induced
19	6	28.6	4	2	T30569	hypothetical prote
20	6	28.6	4	2	I38888	COI intron 16 prot
21	6	28.6	4	2	JQ1273	neuropeptide Antho
22	6	28.6	4	2	A35779	neuropeptide Antho
23	6	28.6	4	2	A25844	autho-RF amide neu
24	6	28.6	4	2	A60418	FMRFamide - polych
25	6	28.6	4	2	A34626	RPCH-related neuro
26	6	28.6	4	2	A32480	achatin-1 - giant
27	6	28.6	4	2	S39390	myosin-light-chain
28	6	28.6	4	2	PT0271	Ig heavy chain CRD
29	6	28.6	4	2	S43959	Ig mu chain V regi

ALIGNMENTS

RESULT 1

PT0240  
Ig heavy chain CRD3 region (clone 2-100B) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
C:Accession: PT0240  
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
J. Exp. Med. 173, 395-407, 1991  
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J  
A:Reference number: PT0222; MUID:91108337; PMID:1899102  
A:Accession: PT0240  
A:Molecule type: DNA  
A:Residues: 1-4 <YAM>  
A:Experimental source: B lymphocyte  
C:Keywords: heterotetramer; immunoglobulin

Query Match 47.6%; Score 10; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GL 3  
DB 3 GL 4

RESULT 2

A53284  
T-cell receptor beta 2 chain D region, Dbeta2 - rabbit  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C:Date: 02-May-1994 #sequence\_revision 18-Nov-1994 #text\_change 05-Nov-1999  
C:Accession: A53284  
R:Harindranath, N.; Alexander, C.B.; Mage, R.G.  
Mol. Immunol. 28, 881-888, 1991  
A:Title: Evolutionarily conserved organization and sequences of germline diversity and J  
A:Reference number: A53284; MUID:91342695; PMID:1678859  
A:Accession: A53284  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-4 <HAR>  
A:Cross-references: GB:S60737; NID:G233916; PIDN:AAB19517.1; PID:G233917  
A>Note: sequence extracted from NCBI backbone (NCBIN:60737; NCBIP:60739)  
C:Keywords: T-cell receptor

Query Match 47.6%; Score 10; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GL 3  
DB 1 GL 2

30 6 28.6 4 2 PT0711 T-cell receptor be  
31 6 28.6 4 2 PT0698 T-cell receptor be  
32 6 28.6 4 2 PT0677 T-cell receptor be  
33 6 28.6 4 2 PT0706 T-cell receptor be  
34 6 28.6 4 2 PT0675 T-cell receptor be  
35 6 28.6 4 2 PT0721 T-cell receptor be  
36 6 28.6 4 2 PT0566 T-cell receptor be  
37 6 28.6 4 2 S47552 ubiquitin - rat  
38 6 28.6 4 2 S09478 globulin IV alpha  
39 5 23.8 3 3 PQ0010 angiotensin-conver  
40 5 23.8 3 3 S13894 histidinol dehydro  
41 5 23.8 3 3 I50412 gene p20K protein  
42 5 23.8 3 3 PT0578 T-cell receptor be  
43 5 23.8 3 3 I78890 tyrosine protein k  
44 5 23.8 3 3 T13892 cytochrome-c oxida  
45 5 23.8 4 2 S18401 thyroglobulin - do

RESULT 3  
PT0633  
T-cell receptor beta chain V-D-J region (120-2C) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C:Accession: PT0633  
R:Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A:Reference number: PT0509; MUID:91277601; PMID:1711558  
A:Accession: PT0633  
A>Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-4 <FEE>  
A:Experimental source: newborn thymus, strain BALB/c  
C:Keywords: T-cell receptor

Query Match 38.1%; Score 8; DB 2; Length 4;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GL 3  
|:  
Db 3 GI 4

RESULT 4  
B23751  
spinal cord peptide SCP-5 - pig  
C:Species: Sus scrofa domestica (domestic pig)  
C>Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001  
C:Accession: B23751  
R:Hsi, K.L.; Chen, R.L.; Chen, Z.G.; Zhang, H.L.; Lu, Y.A.; Guo, S.Y.; Wu, S.X.; Tsou, K.  
Arch. Biochem. Biophys. 240, 178-183, 1985  
A:Reference number: A23751; MUID:85250425; PMID:4015098  
A:Accession: B23751  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-3 <HSI>  
C:Superfamily: unassigned animal peptides

Query Match 33.3%; Score 7; DB 3; Length 3;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 LM 4  
|:  
Db 1 MM 2

RESULT 5  
E44823  
synaptosomal-associated protein SNAP-25 peptide 1 - rabbit (fragment)  
N:Alternate names: superprotein peptide 1  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C>Date: 31-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 15-Jun-1996  
C:Accession: E44823  
R:Loewy, A.; Liu, W.S.; Baitinger, C.; Willard, M.B.  
J. Neurosci. 11, 3412-3421, 1991  
A:Title: The major 35S-methionine-labeled rapidly transported protein (superprotein) is  
A:Reference number: A44823; MUID:92044785; PMID:1941090  
A:Accession: E44823  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-4 <LOE>  
A:Experimental source: visual tissue  
A>Note: sequence extracted from NCBI backbone (NCBIP:64247)  
C:Keywords: membrane trafficking

Query Match 33.3%; Score 7; DB 2; Length 4;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 LM 4  
|:  
Db 1 IM 2

## RESULT 6

B53284  
T-cell receptor beta 2 chain D region, Dbeta2 - rabbit  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C>Date: 02-May-1994 #sequence\_revision 18-Nov-1994 #text\_change 05-Nov-1999  
C:Accession: B53284  
R:Harindranath, N.; Alexander, C.B.; Mage, R.G.  
Mol. Immunol. 28, 881-888, 1991  
A:Title: Evolutionarily conserved organization and sequences of germline diversity and  
A:Reference number: A53284; MUID:91342695; PMID:1678859  
A:Accession: B53284  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-4 <HAR>  
A:Cross-references: GB:S60737; NID:G233916; PIDN:AA19518.1; PID:G233918  
A>Note: sequence extracted from NCBI backbone (NCBIN:60737, NCBIP:60738)  
C:Keywords: T-cell receptor

Query Match 33.3%; Score 7; DB 2; Length 4;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FG 2  
|:  
Db 2 WG 3

## RESULT 7

GKHU  
growth-modulating peptide - human  
C:Species: Homo sapiens (man)  
C>Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001  
C:Accession: A01421  
R:Schlesinger, D.H.; Pickart, L.; Thaler, M.M.  
Experientia 33, 324-325, 1977  
A:Title: Growth-modulating serum tripeptide is glycyl-histidyl-lysine.  
A:Reference number: A01421; MUID:77162369; PMID:858356  
A:Accession: A01421  
A:Molecule type: protein  
A:Residues: 1-3 <SCH>  
A>Note: this serum tripeptide is found to stimulate growth of some cell types and to inhibit  
C:Superfamily: unassigned animal peptides

Query Match 28.6%; Score 6; DB 3; Length 3;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 G 2  
|:  
Db 1 G 1

## RESULT 8

A60898  
bursin - chicken  
C:Species: Gallus gallus (chicken)  
C>Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001  
C:Accession: A60898  
R:Audhya, T.; Kroon, D.; Heavner, G.; Viamontes, G.; Goldstein, G.  
Science 231, 997-999, 1986  
A:Title: Tripeptide structure of bursin, a selective B-cell-differentiating hormone of  
A:Reference number: A60898; MUID:86122916; PMID:3484838  
A:Accession: A60898  
A:Molecule type: protein  
A:Residues: 1-3 <AUD>  
C:Superfamily: unassigned animal peptides  
C:Keywords: amidated carboxyl end; hormone  
F;3/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 28.6%; Score 6; DB 3; Length 3;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 G 2  
|  
Db 3 G 3

## RESULT 9

A23751  
spinal cord peptide SCP-4 - pig  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001  
C:Accession: A23751  
R/Hsi, K.L.; Chen, R.L.; Chen, Z.G.; Zhang, H.L.; Lu, Y.A.; Guo, S.Y.; Wu, S.X.; Tsou, K.  
Arch. Biochem. Biophys. 240, 178-183, 1985  
A:Reference number: A23751; MUID:85250425; PMID:4015098  
A:Accession: A23751  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-3 <HSI>  
C:Superfamily: unassigned animal peptides

Query Match 28.6%; Score 6; DB 3; Length 3;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 G 2  
|  
Db 2 G 2

## RESULT 10

PT0636  
T-cell receptor beta chain V-D-J region (100-2AT) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001  
C:Accession: PT0636  
R:Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A:Reference number: PT0509; MUID:91277601; PMID:1711558  
A:Accession: PT0636  
A:Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-3 <FEE>  
A:Experimental source: newborn thymus, strain BALB/c  
C:Keywords: T-cell receptor

Query Match 28.6%; Score 6; DB 3; Length 3;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 G 2  
|  
Db 3 G 3

## RESULT 11

PT0571  
T-cell receptor beta chain V-D-J region (141-1CM) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001  
C:Accession: PT0571  
R:Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A:Reference number: PT0509; MUID:91277601; PMID:1711558  
A:Accession: PT0571  
A:Status: translation not shown  
A:Molecule type: mRNA

A:Residues: 1-3 <FEE>

A:Experimental source: day 19 fetal thymus, strain BALB/c  
C:Keywords: T-cell receptor

Query Match 28.6%; Score 6; DB 3; Length 3;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 G 2  
|  
Db 3 G 3

## RESULT 12

S68328  
blood cell protein A - Molgula manhattensis (fragment)  
C:Species: Molgula manhattensis  
C:Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001  
C:Accession: S68328  
R:Taylor, S.W.; Ross, M.M.; Waite, J.H.  
Arch. Biochem. Biophys. 324, 228-240, 1995  
A:Title: Novel 3,4-di- and 3,4,5-trihydroxyphenylalanine-containing polypeptides from the  
A:Reference number: S68325; MUID:96132650; PMID:8554314  
A:Accession: S68328  
A:Molecule type: protein  
A:Residues: 1-3 <TAY>

Query Match 28.6%; Score 6; DB 3; Length 3;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
|  
Db 2 F 2

## RESULT 13

ECXAA  
Ancho-RFamide neuropeptide - sea anemone (Anthopleura elegantissima)  
C:Species: Anthopleura elegantissima  
C:Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 08-Dec-1995  
C:Accession: A26666  
R:Grimmelikhuijzen, C.J.P.; Graff, D.  
Proc. Natl. Acad. Sci. U.S.A. 83, 9817-9821, 1986  
A:Title: Isolation of <Glu-Gly-Arg-Phe-NH2 (Ancho-RFamide), a neuropeptide from sea anem  
A:Reference number: A26666; MUID:87092339; PMID:2879288  
A:Accession: A26666  
A:Molecule type: protein  
A:Residues: 1-4 <GRI>  
C:Comment: The function of this peptide is not known but it could act as a transmitter a  
C:Comment: Synthetic and natural peptides had identical properties.  
C:Superfamily: RFamide neuropeptide  
C:Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid  
F:1/Modified site: pyroglutamate carboxylic acid (Gln) #status experimental  
F:4/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 28.6%; Score 6; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 G 2  
|  
Db 2 G 2

## RESULT 14

A32039  
tyrosine-melanocyte-stimulating hormone release-inhibiting factor 1 - bovine  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 31-Jul-1989 #sequence\_revision 31-Jul-1989 #text\_change 18-Aug-2000  
C:Accession: A32039  
R:Horvath, A.; Kastin, A.J.  
J. Biol. Chem. 264, 2175-2179, 1989

A;Title: Isolation of tyrosine-melanocyte-stimulating hormone release-inhibiting factor  
A;Reference number: A32039; MUID:89123285; PMID:2563371  
A;Accession: A32039  
A;Molecule type: protein  
A;Residues: 1-4 <HOR>  
A;Experimental source: brain  
C;Superfamily: unassigned animal peptides  
C;Keywords: amidated carboxyl end  
F;4/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 28.6%; Score 6; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 G 2  
|  
Db 4 G 4

RESULT 15  
ECNK  
cardioexcitatory neuropeptide FMRFamide - sunray clam  
C;Species: Macrocallista nimbosa (sunray clam)  
C;Date: 20-Jun-2000 #sequence\_revision 20-Jun-2000 #text\_change 20-Jun-2000  
C;Accession: A01426  
R;Price, D.A.; Greenberg, M.J.  
Science 157, 670-671, 1977  
A;Title: Structure of a molluscan cardioexcitatory neuropeptide.  
A;Reference number: A01426; MUID:77215956; PMID:877582  
A;Accession: A01426  
A;Molecule type: protein  
A;Residues: 1-4 <PRL>  
A;Note: the active peptide was also synthesized  
C;Comment: This peptide was purified from pooled extracts of cerebral, pedal, and visceral  
action in molluscs; its exact physiological role is not yet established.  
C;Superfamily: unassigned animal peptides  
C;Keywords: amidated carboxyl end; neuropeptide  
F;4/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 28.6%; Score 6; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
|  
Db 1 F 1

Search completed: August 25, 2004, 14:25:25  
Job time : 39 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 25, 2004, 14:16:24 ; Search time 22 Seconds  
(without alignments)  
9.467 Million cell updates/sec

Title: US-10-053-669-2  
Perfect score: 21  
Sequence: 1 FGLM 4

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 18

Minimum DB seq length: 0  
Maximum DB seq length: 4

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	12	57.1	4	1	OCPI_OCTMI
2	6	28.6	3	1	GRWM_HUMAN
3	6	28.6	4	1	ACH1_ACHFU
4	6	28.6	4	1	DCML_PSECH
5	6	28.6	4	1	EOST_HUMAN
6	6	28.6	4	1	FAR3_HIRME
7	6	28.6	4	1	FAR4_HIRME
8	6	28.6	4	1	FFKA_ANTEL
9	6	28.6	4	1	FLRN_HIRME
10	6	28.6	4	1	FLRN_ANTEL
11	6	28.6	4	1	FMRP_MACNI
12	6	28.6	4	1	FYRI_ANTEL
13	6	28.6	4	1	OCPI_OCTMI
14	5	23.8	4	1	DCMS_PSECH
15	2	9.5	3	1	LUXE_VIBFI
16	1	4.8	4	1	RM01_YEAST
17	0	0.0	3	1	THYL_PIG
18	0	0.0	4	1	TUFT_HUMAN

## ALIGNMENTS

RESULT 1  
OCPI\_OCTMI STANDARD; PRT; 4 AA.  
AC P58648;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Cardioactive peptides Ocp-1/Ocp-2.  
OS Octopus minor (Octopus).  
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;

OC Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.  
OX NCBI\_TaxID=89766;  
RN [1]  
RP SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.  
RC TISSUE=Brain;  
RX MEDLINE=20336815; PubMed=10876044;  
RA Iwakoshi E., Hisada M., Minakata H.;  
RT "Cardioactive peptides isolated from the brain of a Japanese octopus, Octopus minor.";  
RL Peptides 21:623-630(2000).  
CC -!- FUNCTION: Cardioactive; has both positive chronotropic and inotropic effects on the heart. Ocp-2 is a 1000 time less active than Ocp-1.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- PTM: Ocp-2 has L-Phe instead of D-Phe.  
CC -!- MASS SPECTROMETRY: MW=395.2; METHOD=MALDI.  
KW Hormone; D-amino acid.  
FT MOD\_RES 2 2 D-PHENYLALANINE (IN OCP-1).  
SQ SEQUENCE 4 AA; 394 MW; 6AA879C810000000 CRC64;

Query Match 57.1%; Score 12; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.4e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FG 2  
Db 2 FG 3

## RESULT 2

GRWM\_HUMAN STANDARD; PRT; 3 AA.  
AC P01157;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 21-JUL-1986 (Rel. 01, Last annotation update)  
DE Growth-modulating peptide.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=77162369; PubMed=858356;  
RA Schlesinger D.H., Pickart L., Thaler M.M.;  
RT "Growth-modulating serum tripeptide is glycyl-histidyl-lysine.";  
RL Experientia 33:324-325(1977).  
CC -!- MISCELLANEOUS: This serum tripeptide has been found to stimulate growth of some cell types and to inhibit other types in vitro.  
DR GO: GO:0001558; P:regulation of cell growth; NAS.  
SQ SEQUENCE 3 AA; 340 MW; 6331E81000000000 CRC64;

Query Match 28.6%; Score 6; DB 1; Length 3;  
Best Local Similarity 100.0%; Pred. No. 1.4e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 G 2  
Db 1 G 1

## RESULT 3

ACH1\_ACHFU STANDARD; PRT; 4 AA.  
AC P35904;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 22, Last sequence update)  
DT 15-JUL-1998 (Rel. 36, Last annotation update)  
DE Achatin-I.  
OS Achatina fulica (Giant African snail).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;  
OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.  
OX NCBI\_TaxID=6530;

RN SEQUENCE, CHARACTERIZATION, AND SYNTHESIS.  
 RP STRAIN=Perussac; TISSUE=Ganglion;  
 RX MEDLINE=89273551; PubMed=2597281;  
 RA Kamatani Y., Minakata H., Kenny P.T.M., Iwashita T., Watanabe K.,  
 RA Funase K., Sun X.P., Yonggiri A., Kim K.H., Novales-Li P.,  
 RA Novales E.T., Kanapi C.G., Takeuchi H., Nomoto K.;  
 RT "Achatin-I, an endogenous neuroexcitatory tetrapeptide from Achatina  
 RT fulica Ferussac containing a D-amino acid residue."  
 RL Biochem. Biophys. Res. Commun. 160:1015-1020(1989).  
 RN [2]  
 RP CHARACTERIZATION.  
 RX STRAIN=Perussac; TISSUE=Heart atrium;  
 RX MEDLINE=91264856; PubMed=1675568;  
 RA Fujimoto K., Kubota I., Yasuda-Kamatani Y., Minakata H., Nomoto K.,  
 RA Yoshida M., Harada A., Muneoka Y., Kobayashi M.;  
 RT "Purification of achatin-I from the atria of the African giant snail,  
 RT Achatina fulica, and its possible function."  
 RL Biochem. Biophys. Res. Commun. 177:847-853(1991).  
 RN [3]  
 RP X-RAY CRYSTALLOGRAPHY.  
 RX MEDLINE=93014529; PubMed=1399265;  
 RA Ishida T., In Y., Doi M., Inoue M., Yasuda-Kamatani Y., Minakata H.,  
 RA Iwashita T., Nomoto K.;  
 RT "Crystal structure and molecular conformation of achatin-I  
 RT (H-Gly-D-Phe-Ala-Asp-OH), an endogenous neuropeptide containing a  
 RT D-amino acid residue."  
 RL Int. J. Pept. Protein Res. 39:258-264(1992).  
 CC -I- FUNCTION: Neuroexcitatory peptide; increases the impulse frequency  
 CC and produces a spike broadening of the identified heart excitatory  
 CC neuron (PON); also enhances the amplitude and frequency of the  
 CC heart beat. Has also an effect on several other muscles.  
 DR PIR; A32480; A32480.  
 KW Hormone; D-amino acid.  
 FT MOD RES 2 D-PHENYLALANINE.  
 SQ SEQUENCE 4 AA; 408 MW; 6AADD9C810000000 CRC64;  
 Query Match 28.6%; Score 6; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 G 2  
 Db 1 G 1  
 RESULT 4  
 DCML PSECH STANDARD; PRT; 4 AA.  
 AC P19916;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Carbon monoxide dehydrogenase large chain (EC 1.2.99.2) (CO  
 DE dehydrogenase subunit L) (CO-DH L) (Fragment).  
 GN CUTL  
 OS Pseudomonas carboxydohydrogena.  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Bradyrhizobiaceae.  
 OX NCBI\_TaxID=290;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=90055678; PubMed=2818128;  
 RA Kraut M., Hugendieck I., Herwig S., Meyer O.;  
 RT "Homology and distribution of CO dehydrogenase structural genes in  
 RT carboxydophilic bacteria."  
 RL Arch. Microbiol. 152:335-341(1989).  
 CC -I- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon  
 CC dioxide.  
 CC -I- CATALYTIC ACTIVITY: CO + H(2)O + acceptor = CO(2) + reduced  
 CC acceptor.  
 CC -I- COFACTOR: Molybdenum (molybdopterin).  
 CC -I- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND

CC SMALL.  
 DR PIR; PLO140; PLO140.  
 KW Oxidoreductase; Molybdenum.  
 FT NON TER 4  
 SQ SEQUENCE 4 AA; 441 MW; 7761E876F00000000 CRC64;  
 Query Match 28.6%; Score 6; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 G 2  
 Db 2 G 2  
 RESULT 5  
 EOSI\_HUMAN STANDARD; PRT; 4 AA.  
 ID EOSI\_HUMAN  
 AC P02731;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 21-JUL-1986 (Rel. 01, Last annotation update)  
 DE Eosinophilotoxic peptides.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=76078412; PubMed=1060093;  
 RA Goetzl E.J., Austen K.F.;  
 RT "Purification and synthesis of eosinophilotoxic tetrapeptides of  
 RT human lung tissue: identification as eosinophil chemotactic factor of  
 RT anaphylaxis."  
 RL Proc. Natl. Acad. Sci. U.S.A. 72:4123-4127(1975).  
 CC -I- MISCELLANEOUS: These peptides are released from mast cells in lung  
 CC (and other tissues) during hypersensitivity reactions  
 CC (anaphylaxis). Their activities, preferentially affecting  
 CC eosinophils, include chemotaxis, chemotactic deactivation, release  
 CC of enzymes, and stimulation of the hexose monophosphate shunt.  
 DR GO; GO:0006935; P:chemotaxis; IDA.  
 DR GO; GO:0006955; P:immune response; IDA.  
 FT VARIANT 1 V -> A (IN OTHER PEPTIDE).  
 FT SEQUENCE 4 AA; 390 MW; 6B05B862A00000000 CRC64;  
 Query Match 28.6%; Score 6; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 G 2  
 Db 2 G 2  
 RESULT 6  
 FAR3\_HIRME STANDARD; PRT; 4 AA.  
 ID FAR3\_HIRME  
 AC P42562;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE FMRamide-like neuropeptide YLRP-amide.  
 OS Hirudo medicinalis (Medicinal leech).  
 OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;  
 OC Arhynchobellida; Hirudiniformes; Hirudinidae; Hirudo.  
 OX NCBI\_TaxID=6421;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=92195954; PubMed=1686933;  
 RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;  
 RT "Identification of Rfamide neuropeptides in the medicinal leech."  
 RL Peptides 12:897-908(1991).

CC -!- SIMILARITY: Belongs to the FARP (FMRamide related peptide)  
 CC family.  
 KW Neuropeptide; Amidation.  
 FT MOD RES 4 4 4 AMIDATION.  
 SQ SEQUENCE 4 AA; 598 MW; 69D407B300000000 CRC64;  
 Query Match 28.6%; Score 6; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 F 1  
 Db 4 F 4

RESULT 7  
 FARP4\_HIRME  
 ID FARP4\_HIRME STANDARD; PRT; 4 AA.  
 AC P42563;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE FMRamide-like neuropeptide (FMR-amide).  
 OS Hirudo medicinalis (Medicinal leech).  
 CC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;  
 OC Arhynchobdellida; Hirudiniiformes; Hirudinidae; Hirudo.  
 OX NCBI\_TaxID=6421;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=92195954; PubMed=1686933;  
 RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;  
 RT "Identification of RFamide neuropeptides in the medicinal leech."  
 RL Peptides 12:897-908(1991).  
 CC -!- SIMILARITY: Belongs to the FARP (FMRamide related peptide)  
 CC family.  
 KW Neuropeptide; Amidation.  
 FT MOD RES 4 4 4 AMIDATION.  
 SQ SEQUENCE 4 AA; 616 MW; 69D406B300000000 CRC64;  
 Query Match 28.6%; Score 6; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 F 1  
 Db 4 F 4

RESULT 8  
 FFK4\_ANTEL  
 ID FFK4\_ANTEL STANDARD; PRT; 4 AA.  
 AC P58705;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Antho-Kaamide.  
 OS Anthopleura elegantissima (Sea anemone).  
 CC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;  
 OC Nynanthaeae; Actiniidae; Anthopleura.  
 OX NCBI\_TaxID=6110;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=92028852; PubMed=1681803;  
 RA Nothacker H.-P., Rinehart K.L. Jr., Grimmelikhuijzen C.J.P.;  
 RT "Isolation of L-3-phenyllactyl-Phe-Lys-Ala-NH2 (Antho-Kaamide), a  
 novel neuropeptide from sea anemones."  
 RL Biochem. Biophys. Res. Commun. 179:1205-1211(1991).  
 RN [2]  
 RP FUNCTION.  
 RX MEDLINE=93391436; PubMed=8397415;  
 RA McFarlane I.D., Hudman D., Nothacker H.-P., Grimmelikhuijzen C.J.P.;  
 RT "The expansion behaviour of sea anemones may be coordinated by two  
 inhibitory neuropeptides, Antho-Kaamide and Antho-Riamide.";

RL Proc. R. Soc. Lond., B, Biol. Sci. 253:183-188(1993).  
 CC -!- FUNCTION: Inhibits spontaneous contractions in several muscle  
 CC groups. May be involved in the expansion phase of feeding  
 CC behaviour in sea anemones.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Neuron specific.  
 DR PIR; J01273; J01273.  
 KW Neuropeptide; Amidation.  
 FT MOD RES 1 1 1 L-3-PHENYLACTYL.  
 FT MOD RES 4 4 4 AMIDATION.  
 SQ SEQUENCE 4 AA; 512 MW; 6DD339CA00000000 CRC64;  
 Query Match 28.6%; Score 6; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 F 1  
 Db 1 F 1

RESULT 9  
 FLRF\_HIRME  
 ID FLRF\_HIRME STANDARD; PRT; 4 AA.  
 AC P42561;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE FLRFamide.  
 OS Hirudo medicinalis (Medicinal leech), and  
 OS Helisoma trivolvis (Snail).  
 CC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;  
 OC Arhynchobdellida; Hirudiniiformes; Hirudinidae; Hirudo.  
 OX NCBI\_TaxID=6421, 27815;  
 RN [1]  
 RP SEQUENCE.  
 RC SPECIES=H. medicinalis;  
 RX MEDLINE=92195954; PubMed=1686933;  
 RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;  
 RT "Identification of RFamide neuropeptides in the medicinal leech."  
 RL Peptides 12:897-908(1991).  
 RN [2]  
 RP SEQUENCE.  
 RC SPECIES=H. trivolvis; TISSUE=Kidney;  
 RX MEDLINE=94286417; PubMed=7312428;  
 RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;  
 RT "FMRamide-related peptides from the kidney of the snail, Helisoma  
 trivolvis."  
 RL Peptides 15:31-36(1994).  
 CC -!- SIMILARITY: Belongs to the FARP (FMRamide related peptide)  
 CC family.  
 KW Neuropeptide; Amidation.  
 FT MOD RES 4 4 4 AMIDATION.  
 SQ SEQUENCE 4 AA; 582 MW; 69D40729A000000000 CRC64;  
 Query Match 28.6%; Score 6; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 F 1  
 Db 1 F 1

RESULT 10  
 FLRN\_ANTEL  
 ID FLRN\_ANTEL STANDARD; PRT; 4 AA.  
 AC P58707;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Antho-RNamide.  
 OS Anthopleura elegantissima (Sea anemone).

OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;  
 OC Nynanthaeae; Actiniidae; Anthopleura.  
 OX NCBI\_TaxID=6110;

RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RX MEDLINE=90319122; PubMed=1973541;  
 RA Grimmelikhuijzen C.J.P., Rinehart K.L. Jr., Jacob E., Graff D.,  
 RA Reinscheid K.K., Nothacker H.-P., Staley A.L.;  
 RT "Isolation of L-3-phenylalanyl-Leu-Arg-Asn-NH2 (Antho-RNamide), a sea  
 RT anemone neuropeptide containing an unusual amino-terminal blocking  
 RT group.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 87:5410-5414(1990).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Neuron specific.  
 CC -!- MASS SPECTROMETRY: MW=549.3; METHOD=FAB.  
 DR PIR; A35779; A35779.  
 FT MOD\_RES 1 1 L-3-PHENYLALACTYL.  
 FT MOD\_RES 4 4 AMIDATION.  
 SQ SEQUENCE 4 AA; 549 MW; 64540729A0000000 CRC64;

Query Match 28.6%; Score 6; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
 DB 1 F 1

RESULT 11  
 FMRF MACNI STANDARD; PRT; 4 AA.  
 AC P01162;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE FMRFamide (Peak C) (Cardioexcitatory neuropeptide).  
 OS Macrocallista nimbosa (Sun-ray clam),  
 OS Nereis virens (Sandworm),  
 OS Hirudo medicinalis (Medicinal leech), and  
 OS Helisoma trivolvis (Snail).  
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Heteroconchia; Veneroidea;  
 OC Veneroidea; Veneridae; Macrocallista.  
 OX NCBI\_TaxID=6594, 6353, 6421, 27815;  
 RN [1]  
 RP SEQUENCE, AND SYNTHESIS.  
 RC SPECIES=M.nimbosa; TISSUE=Cerebral pedal, and Visceral ganglion;  
 RX MEDLINE=77215956; PubMed=877582;  
 RA Price D.A., Greenberg M.J.;  
 RT "Structure of a molluscan cardioexcitatory neuropeptide.";  
 RL Science 197:670-671(1977).  
 RN [2]

RP SEQUENCE, AND CHARACTERIZATION.  
 RC SPECIES=M.nimbosa; TISSUE=Ganglion;  
 RX MEDLINE=78012038; PubMed=909875;  
 RA Price D.A., Greenberg M.J.;  
 RT "Purification and characterization of a cardioexcitatory neuropeptide  
 RT from the central ganglia of a bivalve mollusc.";  
 RL Prep. Biochem. 7:261-281(1977).  
 RN [3]  
 RP SEQUENCE.  
 RC SPECIES=N.virens;  
 RX MEDLINE=90259866; PubMed=2342992;  
 RA Krajniak K.G., Price D.A.;  
 RT "Authentic FMRFamide is present in the polychaete Nereis virens.";  
 RL Peptides 11:75-77(1990).  
 RN [4]

RP SEQUENCE.  
 RC SPECIES=H.medicalinalis;  
 RX MEDLINE=92195954; PubMed=1686933;  
 RA Evans B.D., Pohl J., Karlsonis M.A., Calabrese R.L.;  
 RT "Identification of RFamide neuropeptides in the medicinal leech."

RL Peptides 12:897-908(1991).  
 RN [5]  
 RP SEQUENCE.  
 RC SPECIES=H.trivolvis; TISSUE=Kidney;  
 RX MEDLINE=94286417; PubMed=7912428;  
 RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;  
 RT "FMRFamide-related peptides from the kidney of the snail, Helisoma  
 RT trivolvis.";  
 RL Peptides 15:31-36(1994).  
 CC -!- FUNCTION: Myoactive; cardioexcitatory substance. Pharmacological  
 CC activities include augmentation, induction, and regularization of  
 CC cardiac contraction.  
 CC -!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)  
 CC family.  
 DR PIR; A01426; ECNK.  
 DR PIR; A60418; A60418.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 4 4 AMIDATION.  
 SQ SEQUENCE 4 AA; 600 MW; 69D40699A0000000 CRC64;

Query Match 28.6%; Score 6; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
 DB 1 F 1

RESULT 12  
 FYRI ANTEL STANDARD; PRT; 4 AA.  
 AC P58706;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Antho-Riamide I [Contains: Antho-Riamide II].  
 OS Anthopleura elegantissima (Sea anemone).  
 OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;  
 OC Nynanthaeae; Actiniidae; Anthopleura.  
 OX NCBI\_TaxID=6110;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=92270459; PubMed=1821096;  
 RA Nothacker H.-P., Rinehart K.L. Jr., McFarlane I.D.,  
 RA Grimmelikhuijzen C.J.P.;  
 RT "Isolation of two novel neuropeptides from sea anemones: the unusual,  
 RT biologically active L-3-phenylalanyl-Tyr-Arg-Ile-NH2 and its  
 RT des-phenylalanyl fragment Tyr-Arg-Ile-NH2.";  
 RL Peptides 12:1165-1173(1991).  
 RN [2]  
 RP FUNCTION.

RX MEDLINE=93391436; PubMed=8397415;  
 RA McFarlane I.D., Hudman D., Nothacker H.-P., Grimmelikhuijzen C.J.P.;  
 RT "The expansion behaviour of sea anemones may be coordinated by two  
 RT inhibitory neuropeptides, Antho-KAamide and Antho-Riamide.";  
 RL Proc. R. Soc. Lond., B, Biol. Sci. 253:183-188(1993).  
 CC -!- FUNCTION: Inhibits spontaneous contractions in several muscle  
 CC groups. May be involved in the expansion phase of feeding  
 CC behaviour in sea anemones.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Neuron specific.  
 KW Neuropeptide; Amidation.  
 FT CHAIN 1 4 ANTHO-RIAMIDE I.  
 FT CHAIN 2 4 ANTHO-RIAMIDE II.  
 FT MOD\_RES 1 1 L-3-PHENYLALACTYL.  
 FT MOD\_RES 4 4 AMIDATION.  
 SQ SEQUENCE 4 AA; 598 MW; 60441B59A0000000 CRC64;

Query Match 28.6%; Score 6; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 F 1
      1 F 1
Db

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RESULT 13

OCPI3\_OCP3 OCTMI STANDARD; PRT; 4 AA.

AC P58649; DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Cardioactive peptides Ocp-3/Ocp-4.

OS Octopus minor (Octopus).

OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;

OC Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.

OX NCBI\_TaxID=89766;

RN [1]

RP SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.

RC TISSUE=Brain;

RX MEDLINE=20336815; PubMed=10876044;

RA Iwakoshi E., Hisada M., Minakata H.;

RT "Cardioactive peptides isolated from the brain of a Japanese octopus,

RT Octopus minor.";

RL Peptides 21:623-630(2000).

CC -!- FUNCTION: Cardioactive; has both positive chronotropic and

CC inotropic effects on the heart. Ocp-4 is a 1000 time less

CC active than Ocp-3.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- PTM: Ocp-4 has D-Ser instead of L-Ser.

CC -!- MASS SPECTROMETRY: MW=395.2; METHOD=MALDI.

KW Hormone; D-amino acid.

FT MOD RES 2 2 D-SERINE (IN OCP-4).

SQ SEQUENCE 4 AA; 463 MW; 6AB365B810000000 CRC64;

Query Match 28.6%; Score 6; DB 1; Length 4;

Best Local Similarity 100.0%; Pred. No. 1.4e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 G 2

Db 1 G 1

RESULT 14

DCMS\_PSECH STANDARD; PRT; 4 AA.

AC P19918; DT 01-FEB-1991 (Rel. 17, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Carbon monoxide dehydrogenase small chain (EC 1.2.99.2) (CO

DE dehydrogenase subunit S) (CO-DH S) (Fragment).

GN CUTS.

OS Pseudomonas carboxydohydrogena.

OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;

OC Bradyrhizobiaceae.

OX NCBI\_TaxID=290;

RN [1]

RP SEQUENCE.

RX MEDLINE=90055678; PubMed=2818128;

RA Kraut M., Hugendieck I., Herwig S., Meyer O.;

RT "Homology and distribution of CO dehydrogenase structural genes in

RT carboxydohydrophic bacteria.";

RL Arch. Microbiol. 152:335-341(1989).

CC -!- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon

CC dioxide.

CC -!- CATALYTIC ACTIVITY: CO + H(2)O + acceptor = CO(2) + reduced

CC acceptor.

CC -!- COFACTOR: Binds 2 2Fe-2S clusters.

CC -!- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND

CC SMALL.

DR PIR; PL0146; PL0146.

KW Oxidoreductase; Metal-binding; Iron-sulfur; Iron; 2Fe-2S.

FT NON\_TER 4

SQ SEQUENCE 4 AA; 420 MW; 6DD33DD6F0000000 CRC64;

Query Match 23.8%; Score 5; DB 1; Length 4;

Best Local Similarity 100.0%; Pred. No. 1.4e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 M 4

Db 1 M 1

RESULT 15

LUXE\_VIBFI STANDARD; PRT; 3 AA.

AC P24272; DT 01-MAR-1992 (Rel. 21, Created)

DT 01-MAR-1992 (Rel. 21, Last sequence update)

DT 01-OCT-1996 (Rel. 34, Last annotation update)

DE Long-chain-fatty-acid-luciferin-component ligase (EC 6.2.1.19) (Acyl-

DE protein synthetase) (Fragment).

GN LUXE.

OS Vibrio fischeri.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;

OC Vibrionaceae; Vibrio.

OX NCBI\_TaxID=668;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=91072226; PubMed=2254256;

RA Swartzman E., Kapoor S., Graham A.F., Meighen E.A.;

RT "A new Vibrio fischeri lux gene precedes a bidirectional termination

RT site for the lux operon.";

RL J. Bacteriol. 172:6797-6802(1990).

CC -!- FUNCTION: ACRYL-PROTEIN SYNTHETASE ACTIVATES TETRADECANOIC ACID.

CC IT IS A COMPONENT OF THE FATTY ACID REDUCTASE COMPLEX RESPONSIBLE

CC FOR CONVERTING TETRADECANOIC ACID TO THE ALDEHYDE WHICH SERVES AS

CC SUBSTRATE IN THE LUCIFERASE-CATALYZED REACTION.

CC -!- CATALYTIC ACTIVITY: ATP + an acid + protein = AMP + diphosphate +

CC an acyl-protein thioester.

CC -!- PATHWAY: Bioluminescent fatty acid reduction system; second step.

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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL; M62812; -; NOT\_ANNOTATED\_CDS.

KW Luminescence; Ligase.

FT NON\_TER 1 1

SQ SEQUENCE 3 AA; 374 MW; 6AA3303000000000 CRC64;

Query Match 9.5%; Score 2; DB 1; Length 3;

Best Local Similarity 0.0%; Pred. No. 1.4e+05;

Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 L 3

Db 1 I 1

Search completed: August 25, 2004, 14:22:44

Job time : 24 secs

Blank Sheet

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 25, 2004, 14:17:11 ; Search time 112 Seconds  
(without alignments)  
11.269 Million cell updates/sec

Title: US-10-053-669-2  
Perfect score: 21  
Sequence: 1 FGLM 4

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 3

Minimum DB seq length: 0  
Maximum DB seq length: 4

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL.25.\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phage.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_rvirus.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	9	42.9	4	5	P83568
2	6	28.6	2	5	P83570
3	4	19.0	4	11	Q08433

#### ALIGNMENTS

RESULT 1  
ID P83568  
AC P83568; PRELIMINARY; PRT; 4 AA.  
DT 01-JUN-2003 (TRENBLrel. 24, Created)  
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)  
DE Pheromone peptide ILME.

OS Sepia officinalis (Common cuttlefish).  
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;  
OC Decapodiformes; Sepioidae; Sepiidae; Sepia.  
OX NCBI\_TaxID=6610;  
RN [1]  
RP SEQUENCE, SUBCELLULAR LOCATION, TISSUE SPECIFICITY, AND MASS  
RP SPECTROMETRY.  
RC TISSUE=Egg;  
RX PubMed=10944467;  
RA Zatylny C., Gagnon J., Boucaud-Camou E., Henry J.;  
RT "ILME: a waterborne pheromonal peptide released by the eggs of Sepia  
RT officinalis."  
RL Biochem. Biophys. Res. Commun. 275:217-222(2000).  
RN [2]  
RP SEQUENCE.  
RC TISSUE=Egg;  
RX PubMed=12207899;  
RA Zatylny C., Marvin L., Gagnon J., Henry J.;  
RT "Fertilization in Sepia officinalis: the first mollusk sperm-  
RT attracting peptide."  
RL Biochem. Biophys. Res. Commun. 296:1186-1193(2002).  
CC -!- FUNCTION: HAS MYOTROPIC ACTIVITY TARGETING THE GENITAL TRACT.  
CC -!- SUBCELLULAR LOCATION: SECRETED.  
CC -!- TISSUE SPECIFICITY: FOLLICLE, FULLY GROWN OOCYTE AND EGG(EC2).  
CC -!- MASS SPECTROMETRY: MW=505.4; METHOD=MALDI.  
DR GO:0005186; P:pheromone activity; IEA.  
KW Pheromone.  
SQ SEQUENCE 4 AA; 505 MW; 6B16972030000000 CRC64;

Query Match 42.9%; Score 9; DB 5; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1e+06;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LM 4  
DB 2 LM 3

#### RESULT 2

P83570  
ID P83570 PRELIMINARY; PRT; 2 AA.  
AC P83570;  
DT 01-JUN-2003 (TRENBLrel. 24, Created)  
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)  
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)  
DE Neuropeptide GWA.  
OS Sepia officinalis (Common cuttlefish).  
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;  
OC Decapodiformes; Sepioidae; Sepiidae; Sepia.  
OX NCBI\_TaxID=6610;  
RN [1]  
RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND AMIDATION.  
RC TISSUE=Optic lobe;  
RX PubMed=9437704;  
RA Henry J., Favrel P., Boucaud-Camou E.;  
RT "Isolation and identification of a novel Ala-Pro-Gly-Trp-amide-related  
RT peptide inhibiting the motility of the mature oviduct in the  
RT cuttlefish, Sepia officinalis."  
RL Peptides 18:1469-1474(1997).  
CC -!- FUNCTION: REGULATORY NEUROPEPTIDE WITH MYOTROPIC ACTIVITY  
CC TARGETING THE DISTAL OVIDUCT. INHIBITS THE MOTILITY OF THE OVIDUCT  
CC BY DECREASING TONUS, FREQUENCY AND AMPLITUDE OF CONTRACTIONS.  
CC -!- MASS SPECTROMETRY: MW=259.9; METHOD=MALDI.  
DR GO:0007218; P:neuropeptide signaling pathway; IEA.  
KW Neuropeptide; Amidation.  
FT MOD RES 2  
SQ SEQUENCE 2 AA; 261 MW; 7378100000000000 CRC64;

Query Match 28.6%; Score 6; DB 5; Length 2;  
Best Local Similarity 100.0%; Pred. No. 1e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 G 2

Db1 G 1

RESULT 3  
Q08433  
ID Q08433 PRELIMINARY; PRT; 4 AA.  
AC Q08433;  
DT 01-NOV-1996 (TEMBLrel. 01, Created)  
DT 01-NOV-1996 (TEMBLrel. 01, last sequence update)  
DT 01-JUN-2003 (TEMBLrel. 24, last annotation update)  
DE Bilirubin UDP-glucuronosyltransferase (Fragment).  
OS Rattus sp.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10118;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Gunn;  
RX MEDLINE=91282758; PubMed=1840486;  
RA Sato H., Aono S., Kashiwamata S., Koiwai O.;  
RT "Genetic defect of bilirubin UDP-glucuronosyltransferase in the  
RL hyperbilirubinemic Gunn rat.";  
RL Biochem. Biophys. Res. Commun. 177:1161-1164 (1991).  
DR EMBL; S38636; AAB19259.1; -.  
DR GO; GO:0016740; F:transferase activity; IEA.  
KW Transferase.  
FT NON\_TER 1 1  
SQ SEQUENCE 4 AA; 473 MW; 633732C420000000 CRC64;  
  
Query Match 19.0%; Score 4; DB 11; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3 L 3  
Db 3 L 3

Search completed: August 25, 2004, 14:24:45  
Job time : 116 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 25, 2004, 14:24:52 ; Search time 121 Seconds  
(without alignments)  
10.400 Million cell updates/sec

Title: US-10-053-669-2  
Perfect score: 21  
Sequence: 1 FGLM 4

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1297172 seqs, 314612898 residues

Total number of hits satisfying chosen parameters: 7564

Minimum DB seq length: 0  
Maximum DB seq length: 4

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pap:\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pap:\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US05\_NEW\_PUB.pap:\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pap:\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pap:\*
- 6: /cgn2\_6/ptodata/2/pubpaa/ECTUS\_PUBCOMB.pap:\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pap:\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pap:\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pap:\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pap:\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pap:\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pap:\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pap:\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pap:\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pap:\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pap:\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pap:\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	4	14	US-10-230-133-3
2	21	100.0	4	14	US-10-053-669-2
3	21	100.0	4	16	US-10-695-536-3
4	16	76.2	4	9	US-09-879-442A-9
5	15	71.4	3	14	US-10-230-133-2
6	15	71.4	3	16	US-10-695-536-2
7	14	66.7	4	9	US-09-879-442A-8
8	14	66.7	4	15	US-10-137-867-328
9	13	61.9	4	9	US-09-879-442A-98
10	13	61.9	4	9	US-09-879-442A-99
11	13	61.9	4	9	US-09-943-123-24
12	13	61.9	4	14	US-10-087-905-30
13	13	61.9	4	14	US-10-087-942-30
14	13	61.9	4	14	US-10-087-402-10
15	13	61.9	4	14	US-10-083-894-31

16	13	61.9	4	14	US-10-196-394-98	Sequence 98, Appl
17	13	61.9	4	14	US-10-202-824-11	Sequence 11, Appl
18	13	61.9	4	15	US-10-359-363A-104	Sequence 104, Appl
19	12	57.1	3	14	US-10-121-857-6	Sequence 6, Appl
20	12	57.1	3	14	US-10-255-679-3	Sequence 3, Appl
21	12	57.1	3	14	US-10-208-018-6	Sequence 6, Appl
22	12	57.1	3	14	US-10-104-307-3	Sequence 3, Appl
23	12	57.1	4	8	US-08-484-409-14	Sequence 14, Appl
24	12	57.1	4	8	US-08-484-409-25	Sequence 25, Appl
25	12	57.1	4	9	US-09-804-733A-24	Sequence 24, Appl
26	12	57.1	4	9	US-09-803-126-20	Sequence 20, Appl
27	12	57.1	4	10	US-09-726-470A-29	Sequence 29, Appl
28	12	57.1	4	10	US-09-563-222-1	Sequence 1, Appl
29	12	57.1	4	10	US-09-811-945-15	Sequence 15, Appl
30	12	57.1	4	12	US-10-435-751-98	Sequence 98, Appl
31	12	57.1	4	13	US-10-007-761-62	Sequence 62, Appl
32	12	57.1	4	13	US-10-044-034-1	Sequence 1, Appl
33	12	57.1	4	13	US-10-044-034-25	Sequence 25, Appl
34	12	57.1	4	13	US-10-076-421-3	Sequence 3, Appl
35	12	57.1	4	14	US-10-087-905-14	Sequence 14, Appl
36	12	57.1	4	14	US-10-087-905-17	Sequence 17, Appl
37	12	57.1	4	14	US-10-255-679-5	Sequence 5, Appl
38	12	57.1	4	14	US-10-255-679-2	Sequence 2, Appl
39	12	57.1	4	14	US-10-255-679-11	Sequence 11, Appl
40	12	57.1	4	14	US-10-255-679-12	Sequence 12, Appl
41	12	57.1	4	14	US-10-255-679-13	Sequence 13, Appl
42	12	57.1	4	14	US-10-255-679-14	Sequence 14, Appl
43	12	57.1	4	14	US-10-255-679-16	Sequence 16, Appl
44	12	57.1	4	14	US-10-255-679-36	Sequence 36, Appl
45	12	57.1	4	14	US-10-255-679-52	Sequence 52, Appl

#### ALIGNMENTS

RESULT 1  
US-10-230-133-3  
; Sequence 3, Application US/10230133  
; Publication No. US20030040625A1  
; GENERAL INFORMATION:  
; APPLICANT: Wells, Ibert  
; TITLE OF INVENTION: Antagonists of the magnesium binding defect as therapy agents and methods for treatment of abnormal physiological states  
; FILE REFERENCE: 2892-106  
; CURRENT APPLICATION NUMBER: US/10/230,133  
; PRIOR FILING DATE: 2002-08-29  
; PRIOR APPLICATION NUMBER: 09/635,266  
; FILING DATE: 2000-08-09  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 3  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (4)..(4)  
; OTHER INFORMATION: AMIDATION  
US-10-230-133-3

Query Match 100.0%; Score 21; DB 14; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4  
Db 1 FGLM 4

RESULT 2  
US-10-053-669-2  
; Sequence 2, Application US/10053669  
; Publication No. US20030077658A1

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; GENERAL INFORMATION:
; APPLICANT: Wells, Ibert
; TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound Ma
; TITLE OF INVENTION: for Disease Diagnosis
; FILE REFERENCE: N1427-005
; CURRENT APPLICATION NUMBER: US/10/053,669
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 09/265,690
; PRIOR FILING DATE: 1999-03-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (4)..(4)
; OTHER INFORMATION: AMIDATION
;
US-10-053-669-2

Query Match 100.0%; Score 21; DB 14; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGLM 4
Db 1 FGLM 4

RESULT 3
US-10-695-536-3
; Sequence 3, Application US/10695536
; Publication No. US20040110692A1
; GENERAL INFORMATION:
; APPLICANT: Wells, Ibert Clifton
; TITLE OF INVENTION: Antagonists of the Magnesium Binding Defect as Therapeutic Agents
; TITLE OF INVENTION: and Methods for Treatment of Abnormal Physiological States
; FILE REFERENCE: 800812-0008
; CURRENT APPLICATION NUMBER: US/10/695,536
; CURRENT FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: US 10/230,133
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 09/635,266
; PRIOR FILING DATE: 2000-08-09
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (4)..(4)
; OTHER INFORMATION: AMIDATION
;
US-10-695-536-3

Query Match 100.0%; Score 21; DB 16; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGLM 4
Db 1 FGLM 4

RESULT 4
US-09-879-442A-9
; Sequence 9, Application US/09879442A
; Patent No. US20020142955A1
; GENERAL INFORMATION:
; APPLICANT: CORIXA CORPORATION
; APPLICANT: Dubois, Vincent

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QY 2 GLM 4  
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Db 1 GLM 3

## RESULT 6

US-10-695-536-2  
; Sequence 2, Application US/10695536  
; Publication No. US20040110692A1

; GENERAL INFORMATION:  
; APPLICANT: Wells, Ibert Clifton  
; TITLE OF INVENTION: Antagonists of the Magnesium Binding Defect as Therapeutic Agents  
; FILE REFERENCE: 800812-0008  
; CURRENT APPLICATION NUMBER: US/10/695,536  
; PRIOR FILING DATE: 2003-10-28  
; PRIOR APPLICATION NUMBER: US 10/230,133  
; PRIOR FILING DATE: 2002-08-29  
; PRIOR APPLICATION NUMBER: US 09/635,266  
; PRIOR FILING DATE: 2000-08-09  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2  
; LENGTH: 3  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MOD RES  
; LOCATION: (3)..(3)  
; OTHER INFORMATION: AMIDATION

US-10-695-536-2

Query Match 71.4%; Score 15; DB 16; Length 3;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0

QY 2 GLM 4  
|||  
Db 1 GLM 3

## RESULT 7

US-09-879-442A-8  
; Sequence 8, Application US/09879442A  
; Patent No. US20020142955A1

; GENERAL INFORMATION:  
; APPLICANT: CORIXA CORPORATION  
; APPLICANT: Dubois, Vincent  
; APPLICANT: Fernandez, Anne Marie  
; APPLICANT: Gangwar, Sanjeev  
; APPLICANT: Lewis, Evan  
; APPLICANT: Lobl, Thomas J.  
; APPLICANT: Nieder, Matthew H.  
; APPLICANT: Pickford, Lesley B.  
; APPLICANT: Trouet, Andre  
; APPLICANT: Yarranton, Geoffrey T.  
; TITLE OF INVENTION: ENZYME CLEAVABLE PRODRUG COMPOUNDS  
; FILE REFERENCE: COUL-015/02US  
; CURRENT APPLICATION NUMBER: US/09/879,442A  
; CURRENT FILING DATE: 2001-06-11  
; PRIOR APPLICATION NUMBER: 60/290,448  
; PRIOR FILING DATE: 2001-05-11  
; PRIOR APPLICATION NUMBER: 60/211,887  
; PRIOR FILING DATE: 2000-06-14  
; PRIOR APPLICATION NUMBER: PCT/US99/30393  
; PRIOR FILING DATE: 1999-12-10  
; PRIOR APPLICATION NUMBER: 60/119,312  
; PRIOR FILING DATE: 1999-02-08  
; PRIOR APPLICATION NUMBER: 60/111,793  
; PRIOR FILING DATE: 1998-12-11  
; NUMBER OF SEQ ID NOS: 103  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 8

; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; NAME/KEY: SITE  
; LOCATION: (1)  
; OTHER INFORMATION: Beta-Alanine  
US-09-879-442A-8

Query Match 66.7%; Score 14; DB 9; Length 4;  
Best Local Similarity 66.7%; Pred. No. 1.2e+06; Indels 0; Gaps 0;  
Matches 2; Conservative 1; Mismatches 0

QY 1 FGL 3  
|||  
Db 2 FGI 4

## RESULT 8

US-10-137-867-328  
; Sequence 328, Application US/10137867  
; Publication No. US20030207349A1

; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Bersini, Maureen  
; APPLICANT: Deforge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin I.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3330RLC146  
; CURRENT APPLICATION NUMBER: US/10/137,867  
; CURRENT FILING DATE: 2002-05-03  
; Prior Application removed - See Palm or File Wrapper  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 328  
; LENGTH: 379  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-137-867-328

Query Match 66.7%; Score 14; DB 15; Length 4;  
Best Local Similarity 66.7%; Pred. No. 1.2e+06; Indels 0; Gaps 0;  
Matches 2; Conservative 1; Mismatches 0

QY 1 FGL 3  
|||  
Db 2 FGM 4

## RESULT 9

US-09-879-442A-98  
; Sequence 98, Application US/09879442A  
; Patent No. US20020142955A1

; GENERAL INFORMATION:  
; APPLICANT: CORIXA CORPORATION  
; APPLICANT: Dubois, Vincent  
; APPLICANT: Fernandez, Anne Marie  
; APPLICANT: Gangwar, Sanjeev  
; APPLICANT: Lewis, Evan

```
; APPLICANT: Lobl, Thomas J.
; APPLICANT: Nieder, Matthew H.
; APPLICANT: Pickford, Lesley B.
; APPLICANT: Trouet, Andre
; APPLICANT: Yarranton, Geoffrey T.
; TITLE OF INVENTION: ENZYME CLEAVABLE PRODRUG COMPOUNDS
; FILE REFERENCE: COUL-015/0205
; CURRENT APPLICATION NUMBER: US/09/879,442A
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 60/290,448
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/211,887
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: PCT/US99/30393
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: 60/119,312
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 60/111,793
; PRIOR FILING DATE: 1998-12-11
; NUMBER OF SEQ ID NOS: 103
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 98
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: 2-Thienylalanine
; US-09-879-442A-98

Query Match 61.9%; Score 13; DB 9; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGL 3
Db 2 YGL 4

RESULT 10
US-09-879-442A-99
; Sequence 99, Application US/09879442A
; Patent No. US20020142955A1
; GENERAL INFORMATION:
; APPLICANT: CORIXA CORPORATION
; APPLICANT: Dubois, Vincent
; APPLICANT: Fernandez, Anne Marie
; APPLICANT: Gangwar, Sanjeev
; APPLICANT: Lewis, Evan
; APPLICANT: Lobl, Thomas J.
; APPLICANT: Nieder, Matthew H.
; APPLICANT: Pickford, Lesley B.
; APPLICANT: Trouet, Andre
; APPLICANT: Yarranton, Geoffrey T.
; TITLE OF INVENTION: ENZYME CLEAVABLE PRODRUG COMPOUNDS
; FILE REFERENCE: COUL-015/0205
; CURRENT APPLICATION NUMBER: US/09/879,442A
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 60/290,448
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/211,887
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: PCT/US99/30393
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: 60/119,312
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 60/111,793
; PRIOR FILING DATE: 1998-12-11
; NUMBER OF SEQ ID NOS: 103
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 99

Query Match 61.9%; Score 13; DB 9; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGL 3
Db 2 YGL 4

RESULT 11
US-09-943-123-24
; Sequence 24, Application US/09943123
; Publication No. US20020182701A1
; GENERAL INFORMATION:
; APPLICANT: CHANG, Y-H
; APPLICANT: VETRO, J.A.
; APPLICANT: MICKA, W.S.
; TITLE OF INVENTION: Dominant Negative Variants of Methionine Aminopeptidase
; TITLE OF INVENTION: 2 ("MetAP2") and Clinical Uses Therefor
; FILE REFERENCE: 16153-8007
; CURRENT APPLICATION NUMBER: US/09/943,123
; CURRENT FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: Peptide
; US-09-943-123-24

Query Match 61.9%; Score 13; DB 9; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GLM 4
Db 2 GMM 4

RESULT 12
US-10-087-905-30
; Sequence 30, Application US/10087905
; Publication No. US20030022152A1
; GENERAL INFORMATION:
; APPLICANT: Haaland, Perry D.
; APPLICANT: Sherman, Douglas B.
; APPLICANT: Stewart II, Walter W.
; APPLICANT: Lloyd, Sheila A.
; APPLICANT: Campbell, Robert L.
; TITLE OF INVENTION: METHODS, APPARATUS AND COMPUTER PROGRAM PRODUCTS FOR FORMULATING CULTURE MEDIA
; TITLE OF INVENTION: FORMULATING CULTURE MEDIA
; FILE REFERENCE: P3250
; CURRENT APPLICATION NUMBER: US/10/087,905
; CURRENT FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US/09/359,260
; PRIOR FILING DATE: 1999-07-22
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 4
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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: hypothetical
; OTHER INFORMATION: peptide
US-10-087-905-30

Query Match          61.9%; Score 13; DB 14; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGL 3
   |||
Db 2 FGV 4

RESULT 13
US-10-087-942-30
; Sequence 30, Application US/10087942
; Publication No. US20030165808A1
; GENERAL INFORMATION:
; APPLICANT: Haaland, Perry D.
; APPLICANT: Sherman, Douglas B.
; APPLICANT: Stewart II, Walter W.
; APPLICANT: Lloyd, Sheila A.
; APPLICANT: Campbell, Robert L.
; TITLE OF INVENTION: METHODS, APPARATUS AND COMPUTER PROGRAM PRODUCTS FOR
; TITLE OF INVENTION: FORMULATING CULTURE MEDIA
; FILE REFERENCE: P3250
; CURRENT APPLICATION NUMBER: US/10/087,942
; CURRENT FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US/09/359,260
; PRIOR FILING DATE: 1999-07-22
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: hypothetical
; OTHER INFORMATION: peptide
US-10-087-942-30

Query Match          61.9%; Score 13; DB 14; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGL 3
   |||
Db 2 FGV 4

RESULT 14
US-10-087-402-10
; Sequence 10, Application US/10087402
; Publication No. US20030170748A1
; GENERAL INFORMATION:
; APPLICANT: The Iams Company
; APPLICANT: Davenport, Gary Mitchell
; APPLICANT: Matthews, Jamie Clyde
; TITLE OF INVENTION: Compositions and Methods for Increasing Amino Acid Absorption in
; FILE REFERENCE: 1448.009US1
; CURRENT APPLICATION NUMBER: US/10/087,402
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/273,263
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: US 60/344,088
; PRIOR FILING DATE: 2001-12-26
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 4
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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: tetrapeptide
US-10-087-402-10

Query Match          61.9%; Score 13; DB 14; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GLM 4
   |:-|
Db 2 GWM 4

RESULT 15
US-10-083-894-31
; Sequence 31, Application US/10083894
; Publication No. US20030170766A1
; GENERAL INFORMATION:
; APPLICANT: Brown, Michael S.
; APPLICANT: Goldstein, Joseph L.
; APPLICANT: Reiss, Yuval
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
; IDENTIFICATION, CHARACTERIZATION, AND INHIBITION OF
; FARNESYL PROTEIN TRANSFERASE
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/083,894
; FILING DATE: 27-Feb-2002
; CLASSIFICATION: UNKNOWN
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/937,893
; FILING DATE: 18-APR-1991
; APPLICATION NUMBER: US 07/615,713
; FILING DATE: 20-NOV-1990
; APPLICATION NUMBER: US 07/510,706
; FILING DATE: 18-APR-1990
; APPLICATION NUMBER: NOT APPLICABLE
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, David L.
; REGISTRATION NUMBER: 32,165
; REFERENCE/DOCKET NUMBER: UTSD:249/PAR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-320-7200
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-10-083-894-31

Query Match          61.9%; Score 13; DB 14; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY 2 GLM 4  
|:|  
Db 2 GLM 4

Search completed: August 25, 2004, 14:35:49  
Job time : 122 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 25, 2004, 14:20:15 ; Search time 15 Seconds  
(without alignments)  
13.767 Million cell updates/sec

Title: US-10-053-669-2  
Perfect score: 21  
Sequence: 1 FGLM 4

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 11020

Minimum DB seq length: 0  
Maximum DB seq length: 4

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:  
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2: /cgn2\_6/prodata/2/aaa/5B\_COMB.pep.\*  
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4: /cgn2\_6/prodata/2/aaa/6B\_COMB.pep.\*  
5: /cgn2\_6/prodata/2/aaa/PCUS\_COMB.pep.\*  
6: /cgn2\_6/prodata/2/aaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Length	ID	Description
1	21	100.0	4	1 US-08-441-591-63	Sequence 63, Appl
2	21	100.0	4	1 US-08-303-362A-63	Sequence 63, Appl
3	21	100.0	4	1 US-09-265-690C-2	Sequence 2, Appl
4	21	100.0	4	4 US-09-635-266-3	Sequence 3, Appl
5	21	100.0	4	4 US-10-230-133-3	Sequence 3, Appl
6	21	100.0	4	5 PCT-US95-05600-80	Sequence 80, Appl
7	16	76.2	4	2 US-08-747-137-124	Sequence 124, Appl
8	16	76.2	4	3 US-08-722-126A-20	Sequence 20, Appl
9	15	71.4	3	4 US-09-635-266-2	Sequence 2, Appl
10	15	71.4	3	4 US-10-230-133-2	Sequence 2, Appl
11	15	71.4	4	2 US-08-070-301-8	Sequence 8, Appl
12	15	71.4	4	2 US-08-433-401-4	Sequence 4, Appl
13	14	66.7	4	3 US-08-793-701-25	Sequence 25, Appl
14	14	66.7	4	4 US-09-579-264-25	Sequence 25, Appl
15	13	61.9	4	2 US-08-429-964-37	Sequence 37, Appl
16	13	61.9	4	3 US-08-812-586-60	Sequence 60, Appl
17	13	61.9	4	4 US-08-669-656A-11	Sequence 11, Appl
18	13	61.9	4	4 US-09-535-832A-56	Sequence 56, Appl
19	13	61.9	4	4 US-09-665-362A-31	Sequence 31, Appl
20	13	61.9	4	5 PCT-US93-08062-37	Sequence 37, Appl
21	12	57.1	3	1 US-08-343-943-4	Sequence 4, Appl
22	12	57.1	3	2 US-09-060-455-2	Sequence 2, Appl
23	12	57.1	3	4 US-09-150-621-3	Sequence 3, Appl
24	12	57.1	4	1 US-07-657-769B-58	Sequence 58, Appl
25	12	57.1	4	1 US-07-822-924-3	Sequence 3, Appl
26	12	57.1	4	1 US-07-822-924-5	Sequence 5, Appl
27	12	57.1	4	1 US-07-822-924-7	Sequence 7, Appl

Sequence 1, Appl  
Sequence 1, Appl  
Sequence 1, Appl  
Sequence 2, Appl  
Sequence 3, Appl  
Sequence 4, Appl  
Sequence 10, Appl  
Sequence 20, Appl  
Sequence 108, Appl  
Sequence 10, Appl  
Sequence 11, Appl  
Sequence 20, Appl  
Sequence 108, Appl  
Sequence 16, Appl  
Sequence 11, Appl  
Sequence 29, Appl

## ALIGNMENTS

RESULT 1  
US-08-441-591-63  
; Sequence 63, Application US/08441591  
; Patent No. 5637682  
; GENERAL INFORMATION:  
; APPLICANT: NIEUMLANDT, D., GOLD, L. AND WECKER, M.  
; TITLE OF INVENTION: HIGH-AFFINITY  
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIGANDS  
; TITLE OF INVENTION: TO THE TACHIKININ  
; TITLE OF INVENTION: SUBSTANCE P  
; NUMBER OF SEQUENCES: 66  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Swanson & Bratschun, L.L.C.  
; STREET: 8400 E. Prentice Avenue, Suite 200  
; CITY: Englewood  
; STATE: Colorado  
; COUNTRY: USA  
; ZIP: 80111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage  
; COMPUTER: IBM compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WordPerfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/441,591  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/303,362  
; FILING DATE: 9-SEPTEMBER-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/714,131  
; FILING DATE: 10-JUNE-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/931,473  
; FILING DATE: 17-AUGUST-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/117,991  
; FILING DATE: 8-SEPTEMBER 1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/536,428  
; FILING DATE: 11-JUNE-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/964,624  
; FILING DATE: 21-OCTOBER-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Barry J. Swanson  
; REGISTRATION NUMBER: 33,215  
; REFERENCE/DOCKET NUMBER: NEX21/C  
; TELECOMMUNICATION INFORMATION:

Wed Aug 25 14:50:09 2004

TELEPHONE: (303) 793-3333  
TELEFAX: (303) 793-3433  
INFORMATION FOR SEQ ID NO: 63:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-441-591-63

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Query Match      100.0%; Score 21; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy	1	FGLM	4
D <sub>b</sub>	1	FGLM	4

RESULT 2  
US-08-303-362A-63

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; Sequence 63, Application US/08303362A
; Patent No. 5648214
; GENERAL INFORMATION:
; APPLICANT: NIEUWLANDT, D., GOLD, L. AND WECKER, M.
; TITLE OF INVENTION: HIGH-AFFINITY
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIGANDS
; TITLE OF INVENTION: TO THE TACHYKININ
; TITLE OF INVENTION: SUBSTANCE P
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 E. Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA

```

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/303.362A  
FILING DATE: 9-SEPTEMBER-1994

CLASSIFICATION: 435  
PRIOR APPLICATION DATA: 07/714,131  
FILING DATE: 10-JUNE-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/931,473  
FILING DATE: 17-AUGUST-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/117,991  
FILING DATE: 8-SEPTEMBER 1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/536,428  
FILING DATE: 11-JUNE-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/964,624  
FILING DATE: 21-OCTOBER-1992  
ATTORNEY/AGENT INFORMATION:

NAME: Barry J. Swanson  
REGISTRATION NUMBER: 33,211  
REFERENCE/DOCKET NUMBER: N  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 793-3333  
TELEFAX: (303) 793-3433  
INFORMATION FOR SEQ ID NO: 63:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4  
TYPE: amino acid  
STRANDEDNESS: single

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;      TOPOLOGY: linear
US-08-303-362A-63

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Query Match      100.0%; Score 21; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy	1	FGLM	4
Dp	1	FGLM	4

RESULT 3  
US-09-265-690C-2

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1  Sequence 2, Application US/09265690C
2  Patent No. 6322440
3  GENERAL INFORMATION:
4  APPLICANT: Wells, Ibert
5  TITLE OF INVENTION: Method for Detecting Do
6  TITLE OF INVENTION: for Disease Diagnosis
7  FILE REFERENCE: 1427001
8  CURRENT APPLICATION NUMBER: US/09/265,690C
9  CURRENT FILING DATE: 1999-03-10
10 NUMBER OF SEQ ID NOS: 4
11 SOFTWARE: PatentIn version 3.0
12 SEQ ID NO 2
13 LENGTH: 4
14 TYPE: PRT
15 ORGANISM: Homo sapiens
16 FEATURE:
17 NAME/KEY: MOD_RES
18 LOCATION: (4)..(4)
19 OTHER INFORMATION: AMIDATION
20 US-09-265-690C-2

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Query Match 100.0%; Score 21; DB 4; Length 4;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels

QY	1	FGLM	4
Db	1	FGLM	4

RESULT 4  
US-09-635-266-3

Sequence 3, Application US/09635266  
Patent No. 6455734  
GENERAL INFORMATION:  
APPLICANT: Wells, Ibert  
TITLE OF INVENTION: Antagonists of the mac  
TITLE OF INVENTION: methods for treatment  
FILE REFERENCE: N1427-002  
CURRENT APPLICATION NUMBER: US/09/635,266  
CURRENT FILING DATE: 2000-08-09  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 3  
LENGTH: 4  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: MOD\_RES  
LOCATION: (4) . (4)  
OTHER INFORMATION: AMIDATION  
US-09-635-266-3

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Query Match      100.0%; Score 21; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4: Conservative 0; Mismatches 0; Indels
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Qy 1 FGLM 4



```

Db          1 FGLM 4

RESULT 5
US-10-230-133-3
; Sequence 3, Application US/10230133
; Patent No. 6664420
; GENERAL INFORMATION:
; APPLICANT: Wells, Ibert
; TITLE OF INVENTION: Antagonists of the magnesium binding defect as therapy agents and
; TITLE OF INVENTION: methods for treatment of abnormal physiological states
; FILE REFERENCE: 2892-106
; CURRENT APPLICATION NUMBER: US/10/230,133
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 09/635,266
; PRIOR FILING DATE: 2000-08-09
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 3
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (4)..(4)
; OTHER INFORMATION: AMIDATION
US-10-230-133-3

Query Match          100.0%; Score 21; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 FGLM 4
Db          1 FGLM 4

RESULT 6
PCT-US95-05600-80
; Sequence 80, Application PC/TUS9505600
; GENERAL INFORMATION:
; APPLICANT: GOLD, LARRY
; APPLICANT: NIEUWLANDT, DAN
; APPLICANT: WECKER, MATTHEW
; APPLICANT: SCHNEIDER, DANIEL J.
; APPLICANT: PEIGON, JULI
; APPLICANT: ALLEN, PATRICK
; APPLICANT: SULLENGER, BRUCE A.
; APPLICANT: DOUDNA, JENNIFER, A.
; TITLE OF INVENTION: HIGH-AFFINITY LIGANDS OF
; TITLE OF INVENTION: INSULIN RECEPTOR ANTIBODIES, TACHYKININ SUBSTANCE
; TITLE OF INVENTION: P. HIV INTEGRASE AND HIV-1 REVERSE TRANSCRIPTASE
; NUMBER OF SEQUENCES: 239
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 E. Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MG
; MEDIUM TYPE: storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/05600
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/238,863
; FILING DATE: 06-MAY-1994

```

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/248,632
; FILING DATE: 24-MAY-1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/303,362
; FILING DATE: 09-SEPTEMBER-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/361,795
; FILING DATE: 21-DECEMBER-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/117,991
; FILING DATE: 08-SEPTEMBER-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/931,473
; FILING DATE: 17-AUGUST-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/964,624
; FILING DATE: 21-OCTOBER-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/536,428
; FILING DATE: 11-JUNE-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/714,131
; FILING DATE: 10-JUNE-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/536,428
; FILING DATE: 11-JUNE-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NEX17/PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
PCT-US95-05600-80

Query Match          100.0%; Score 21; DB 5; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 FGLM 4
Db          1 FGLM 4

RESULT 7
US-08-747-137-124
; Sequence 124, Application US/08747137
; Patent No. 5945033
; GENERAL INFORMATION:
; APPLICANT: YEN, Richard C.K.
; TITLE OF INVENTION: NON-CROSSLINKED PROTEIN PARTICLES FOR
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC USE
; NUMBER OF SEQUENCES: 184
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30

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;;  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/747,137  
;; FILING DATE: 12-NOV-1996  
;; CLASSIFICATION: 424  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/212,546  
;; FILING DATE: 14-MAR-1994  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/069,831  
;; FILING DATE: 01-JUN-1993  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/959,560  
;; FILING DATE: 13-OCT-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/641,720  
;; FILING DATE: 15-JAN-1991  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Apple, Randolph T.  
;; REGISTRATION NUMBER: 36,429  
;; REFERENCE/DOCKET NUMBER: 016197-000840US  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 415-576-0200  
;; INFORMATION FOR SEQ ID NO: 124:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 4 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: not relevant  
;; TOPOLOGY: not relevant  
;; FEATURE:  
;; NAME/KEY: Modified-site  
;; LOCATION: 4  
;; OTHER INFORMATION: /product= "Met-Amide"  
;;  
US-08-747-137-124  
  
Query Match 76.2%; Score 16; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 3e+05; 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 FGL 3  
|||  
Db 1 FGL 3  
  
RESULT 8  
US-08-722-126A-20  
; Sequence 20, Application US/08722126A  
; Patent No. 6034227  
; GENERAL INFORMATION:  
; APPLICANT: PECHT, Israel  
; APPLICANT: GUTHMANN, Marcelo D.  
; APPLICANT: TAL, Michael  
; TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL  
; TITLE OF INVENTION: FUNCTION-ASSOCIATED ANTIGEN (MAFA)  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.  
; STREET: 419 Seventh Street N.W., Ste. 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: UNITED STATES OF AMERICA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/722,126A  
; FILING DATE: 08-OCT-1996  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/04258  
; FILING DATE: 06-APR-1995  
  
;;  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: IL 109257  
;; FILING DATE: 08-APR-1994  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: BROWDY, Roger L.  
;; REGISTRATION NUMBER: 25,618  
;; REFERENCE/DOCKET NUMBER: PECHT=1A  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (202) 628-5197  
;; TELEFAX: (202) 737-3528  
;; INFORMATION FOR SEQ ID NO: 20:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 4 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; US-08-722-126A-20  
  
Query Match 76.2%; Score 16; DB 3; Length 4;  
Best Local Similarity 100.0%; Pred. No. 3e+05; 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 FGL 3  
|||  
Db 2 FGL 4  
  
RESULT 9  
US-09-635-266-2  
; Sequence 2, Application US/09635266  
; Patent No. 6455734  
; GENERAL INFORMATION:  
; APPLICANT: Wells, Ibert  
; TITLE OF INVENTION: Antagonists of the magnesium binding defect as therapy agents and  
; TITLE OF INVENTION: methods for treatment of abnormal physiological states  
; FILE REFERENCE: N1427-002  
; CURRENT APPLICATION NUMBER: US/09/635,266  
; CURRENT FILING DATE: 2000-08-09  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2  
; LENGTH: 3  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MOD RES  
; LOCATION: (3)..(3)  
; OTHER INFORMATION: AMIDATION  
; US-09-635-266-2  
  
Query Match 71.4%; Score 15; DB 4; Length 3;  
Best Local Similarity 100.0%; Pred. No. 3e+05; 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 GLM 4  
|||  
Db 1 GLM 3  
  
RESULT 10  
US-10-230-133-2  
; Sequence 2, Application US/10230133  
; Patent No. 6664420  
; GENERAL INFORMATION:  
; APPLICANT: Wells, Ibert  
; TITLE OF INVENTION: Antagonists of the magnesium binding defect as therapy agents and  
; TITLE OF INVENTION: methods for treatment of abnormal physiological states  
; FILE REFERENCE: 2892-106  
; CURRENT APPLICATION NUMBER: US/10/230,133  
; CURRENT FILING DATE: 2002-08-29  
; PRIOR APPLICATION NUMBER: 09/635,266  
; PRIOR FILING DATE: 2000-08-09

;;  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/747,137  
;; FILING DATE: 12-NOV-1996  
;; CLASSIFICATION: 424  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/212,546  
;; FILING DATE: 14-MAR-1994  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/069,831  
;; FILING DATE: 01-JUN-1993  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/959,560  
;; FILING DATE: 13-OCT-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/641,720  
;; FILING DATE: 15-JAN-1991  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Apple, Randolph T.  
;; REGISTRATION NUMBER: 36,429  
;; REFERENCE/DOCKET NUMBER: 016197-000840US  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 415-576-0200  
;; INFORMATION FOR SEQ ID NO: 124:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 4 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: not relevant  
;; TOPOLOGY: not relevant  
;; FEATURE:  
;; NAME/KEY: Modified-site  
;; LOCATION: 4  
;; OTHER INFORMATION: /product= "Met-Amide"  
;;  
US-08-747-137-124  
  
Query Match 76.2%; Score 16; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 3e+05; 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 FGL 3  
|||  
Db 1 FGL 3  
  
RESULT 8  
US-08-722-126A-20  
; Sequence 20, Application US/08722126A  
; Patent No. 6034227  
; GENERAL INFORMATION:  
; APPLICANT: PECHT, Israel  
; APPLICANT: GUTHMANN, Marcelo D.  
; APPLICANT: TAL, Michael  
; TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL  
; TITLE OF INVENTION: FUNCTION-ASSOCIATED ANTIGEN (MAFA)  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.  
; STREET: 419 Seventh Street N.W., Ste. 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: UNITED STATES OF AMERICA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/722,126A  
; FILING DATE: 08-OCT-1996  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/04258  
; FILING DATE: 06-APR-1995

1 NUMBER OF SEQ ID NOS: 4  
2 SOFTWARE: PatentIn version 3.0  
3 SEQ ID NO 2  
4 LENGTH: 3  
5 TYPE: PRT  
6 ORGANISM: Homo sapiens  
7 FEATURE:  
8 NAME/KEY: MOD RES  
9 LOCATION: (3)-(3)  
10 OTHER INFORMATION: AMIDATION  
11 US-10-230-133-2

Query Match 71.4%; Score 15; DB 4; Length 3;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GLM 4  
Db 1 GLM 3

RESULT 11  
US-08-070-301-8  
1 Sequence 8, Application US/08070301  
2 Patent No. 5871995  
3 GENERAL INFORMATION:  
4 APPLICANT: IIDA, Toshio  
5 APPLICANT: KAMINUMA, Toshihiko  
6 APPLICANT: FUSE, Yuka  
7 APPLICANT: TAJIMA, Masahiro  
8 APPLICANT: YANAGI, Mitsuo  
9 APPLICANT: OKAMOTO, Hiroshi  
10 APPLICANT: KISHIMOTO, Jiro  
11 APPLICANT: IFUKU, Ohji  
12 APPLICANT: KATO, Ichiro  
13 TITLE OF INVENTION: ENZYME PARTICIPATING IN C-TERMINAL  
14 TITLE OF INVENTION: AMIDATION, AND METHOD OF PREPARING SAME AND USE THEREOF  
15 NUMBER OF SEQUENCES: 21  
16 CORRESPONDENCE ADDRESS:  
17 ADDRESSEE: Wegner, Cantor, Mueller & Player, P.C.  
18 STREET: 1233 20th Street, N.W.  
19 CITY: Washington  
20 STATE: D.C.  
21 COUNTRY: U.S.A.  
22 ZIP: 20036-8218  
23 COMPUTER READABLE FORM:  
24 MEDIUM TYPE: Floppy disk  
25 COMPUTER: IBM PC compatible  
26 OPERATING SYSTEM: PC-DOS/MS-DOS  
27 SOFTWARE: PatentIn Release #1.0, Version #1.25  
28 CURRENT APPLICATION DATA:  
29 APPLICATION NUMBER: US/08/070,301  
30 FILING DATE: 24-MAY-1991  
31 CLASSIFICATION: 435  
32 PRIOR APPLICATION DATA:  
33 APPLICATION NUMBER: JP 1-209687  
34 FILING DATE: 15-AUG-1989  
35 PRIOR APPLICATION DATA:  
36 APPLICATION NUMBER: JP 1-181933  
37 FILING DATE: 31-OCT-1989  
38 PRIOR APPLICATION DATA:  
39 APPLICATION NUMBER: JP 2-76331  
40 FILING DATE: 26-MAR-1990  
41 PRIOR APPLICATION DATA:  
42 APPLICATION NUMBER: JP 2-106412  
43 FILING DATE: 24-APR-1990  
44 PRIOR APPLICATION DATA:  
45 APPLICATION NUMBER: JP 2-205475  
46 FILING DATE: 02-AUG-1990  
47 ATTORNEY/AGENT INFORMATION:  
48 NAME: Player, William E.  
49 REGISTRATION NUMBER: 31,409  
50 REFERENCE/DOCKET NUMBER: P-450-22830

1 TELECOMMUNICATION INFORMATION:  
2 TELEPHONE: (202) 887-040  
3 TELEFAX: (202) 835-0605  
4 TELEX: 440706  
5 INFORMATION FOR SEQ ID NO: 8:  
6 SEQUENCE CHARACTERISTICS:  
7 LENGTH: 4 amino acids  
8 TYPE: amino acid  
9 STRANDEDNESS: single  
10 TOPOLOGY: linear  
11 MOLECULE TYPE: peptide  
12 US-08-070-301-8

Query Match 71.4%; Score 15; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GLM 4  
Db 1 GLM 3

RESULT 12  
US-08-433-401-4  
1 Sequence 4, Application US/08433401  
2 Patent No. 5872097  
3 GENERAL INFORMATION:  
4 APPLICANT: Ph lenhag, Karin I.  
5 APPLICANT: Fryklund, Linda  
6 APPLICANT: Larsson, Bo C.  
7 APPLICANT: Nyberg, Fred J.  
8 APPLICANT: Westin-Sj dahl, Gertrud E.  
9 APPLICANT: Ludin, Ronny  
10 TITLE OF INVENTION: New Oligopeptides with Affinity to  
11 NUMBER OF SEQUENCES: 4  
12 CORRESPONDENCE ADDRESS:  
13 ADDRESSEE: Pollock, Vande Sande & Priddy  
14 STREET: 1990 M Street, N.W., Suite 800  
15 CITY: Washington  
16 STATE: D.C.  
17 COUNTRY: US  
18 ZIP: 20036-0088  
19 COMPUTER READABLE FORM:  
20 MEDIUM TYPE: Floppy disk  
21 COMPUTER: IBM PC compatible  
22 OPERATING SYSTEM: PC-DOS/MS-DOS  
23 SOFTWARE: PatentIn Release #1.0, Version #1.30  
24 CURRENT APPLICATION DATA:  
25 APPLICATION NUMBER: US/08/433,401  
26 FILING DATE: 18-MAY-1995  
27 CLASSIFICATION: 514  
28 PRIOR APPLICATION DATA:  
29 APPLICATION NUMBER: PCT/SE93/00986  
30 FILING DATE: 18-NOV-1993  
31 PRIOR APPLICATION DATA:  
32 APPLICATION NUMBER: SE 9203496-6  
33 FILING DATE: 20-NOV-1992  
34 ATTORNEY/AGENT INFORMATION:  
35 NAME: Amernick, Burton A.  
36 REGISTRATION NUMBER: 24,852  
37 REFERENCE/DOCKET NUMBER: 151/00118  
38 TELECOMMUNICATION INFORMATION:  
39 TELEPHONE: (202) 331-7111  
40 TELEFAX: (202) 223-2596  
41 INFORMATION FOR SEQ ID NO: 4:  
42 SEQUENCE CHARACTERISTICS:  
43 LENGTH: 4 amino acids  
44 TYPE: amino acid  
45 STRANDEDNESS:  
46 TOPOLOGY: linear  
47 MOLECULE TYPE: peptide  
48 US-08-433-401-4

Query Match 71.4%; Score 15; DB 2; Length 4;  
Best Local Similarity 50.0%; Pred. No. 3e+05;  
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4  
:|:|:  
Db 1 YGLL 4

RESULT 13  
US-08-793-701-25  
; Sequence 25, Application US/08793701  
; Patent No. 6248581  
; GENERAL INFORMATION:  
; APPLICANT: GICQUEL, Brigitte  
; APPLICANT: LIM, Eng Mong  
; APPLICANT: PORTNOI, Denis  
; APPLICANT: BERTHET, Francois-Xavier  
; APPLICANT: TIMM, Juliano  
; TITLE OF INVENTION: MYCOBACTERIA FUNCTIONAL SCREENING AND/OR  
; TITLE OF INVENTION: EXPRESSION VECTORS  
; NUMBER OF SEQUENCES: 63  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: c/o FINNEGAN, HENDERSON, FARRABOW, GARRETT &  
; STREET: 1300 I Street, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/793,701  
; FILING DATE: 09-JUN-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/FR9501133  
; FILING DATE: 30-AUG-1995  
; PRIOR APPLICATION DATA: FR 94/10585  
; APPLICATION NUMBER: FR 94/10585  
; FILING DATE: 02-SEP-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McDonnell, Leslie A.  
; REGISTRATION NUMBER: 34,872  
; REFERENCE/DOCKET NUMBER: 02356.0075  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 408-4400  
; TELEFAX: (202) 408-4400  
; INFORMATION FOR SEQ ID NO: 25:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-793-701-25

Query Match 66.7%; Score 14; DB 3; Length 4;  
Best Local Similarity 66.7%; Pred. No. 3e+05;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGL 3  
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Db 2 FGI 4

RESULT 14  
US-09-579-264-25  
; Sequence 25, Application US/09579264

Query Match 66.7%; Score 14; DB 4; Length 4;  
Best Local Similarity 66.7%; Pred. No. 3e+05;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGL 3  
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Db 2 FGI 4

RESULT 15  
US-08-429-964-37  
; Sequence 37, Application US/08429964  
; Patent No. 5962243  
; GENERAL INFORMATION:  
; APPLICANT: BROWN, MICHAEL S.  
; APPLICANT: GOLDSTEIN, JOSEPH L.  
; APPLICANT: REISS, YUVAL  
; APPLICANT: JAMES, GUY L.  
; TITLE OF INVENTION: METHODS FOR THE IDENTIFICATION OF FARNESYL  
; TITLE OF INVENTION: TRANSFERASE INHIBITORS  
; NUMBER OF SEQUENCES: 85  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ARNOLD, WHITE & DURKEE  
; STREET: P.O. BOX 4433  
; CITY: HOUSTON

Query Match 66.7%; Score 14; DB 4; Length 4;  
Best Local Similarity 66.7%; Pred. No. 3e+05;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGL 3  
:|:|:  
Db 2 FGI 4

RESULT 15  
US-08-429-964-37  
; Sequence 37, Application US/08429964  
; Patent No. 5962243  
; GENERAL INFORMATION:  
; APPLICANT: BROWN, MICHAEL S.  
; APPLICANT: GOLDSTEIN, JOSEPH L.  
; APPLICANT: REISS, YUVAL  
; APPLICANT: JAMES, GUY L.  
; TITLE OF INVENTION: METHODS FOR THE IDENTIFICATION OF FARNESYL  
; TITLE OF INVENTION: TRANSFERASE INHIBITORS  
; NUMBER OF SEQUENCES: 85  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ARNOLD, WHITE & DURKEE  
; STREET: P.O. BOX 4433  
; CITY: HOUSTON

STATE: TEXAS  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/429,964  
FILING DATE: 27-APR-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/021,625  
FILING DATE: 16-FEB-1993  
CLASSIFICATION: 435  
APPLICATION NUMBER: US 07/822,011  
FILING DATE: ABANDONED  
CLASSIFICATION: 435  
APPLICATION NUMBER: PCT/US/91/02650  
FILING DATE: 18-APR-1991  
CLASSIFICATION: 435  
APPLICATION NUMBER: US 07/615,715  
FILING DATE: 20-NOV-1990  
CLASSIFICATION: 435  
APPLICATION NUMBER: US 07/510,706  
FILING DATE: 18-APR-1990 (ABANDONED)  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: PARKER, DAVID L.  
REGISTRATION NUMBER: 32,165  
REFERENCE/DOCKET NUMBER: UTSD:432/PAR  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (512) 418-3000  
TELEFAX: (713) 789-2679  
TELEX: 79-0924  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-429-964-37

Query Match 61.9%; Score 13; DB 2; Length 4;  
Best Local Similarity 66.7%; Pred No. 3e+05;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GLM 4  
|:  
Db 2 GIM 4

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Job time : 16 secs

Blank Sheet

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 25, 2004, 13:57:37 ; Search time 39 Seconds  
(without alignments)  
9.866 Million cell updates/sec

Title: US-10-053-669-2

Perfect score: 21

Sequence: 1 FGLM 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 78:\*

2: pir1:\*

3: pir2:\*

4: pir3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	11	1 SPHO	substance P - hors
2	21	100.0	11	1 A60654	substance P - guin
3	21	100.0	11	2 UN0023	substance P - chic
4	21	100.0	11	2 F60409	substance P-like p
5	21	100.0	11	2 E60409	substance P-like p
6	21	100.0	11	2 S23308	substance P - rain
7	21	100.0	11	2 S33300	probable substance
8	21	100.0	19	2 PS0332	phospholipase A2 (
9	21	100.0	56	2 A69983	hypothetical prote
10	21	100.0	63	2 JC2412	tachykinin gamma c
11	21	100.0	69	2 S04666	hypothetical prote
12	21	100.0	72	2 I62742	tachykinin A gamma
13	21	100.0	72	2 JC5455	prepro-tachykinin-A
14	21	100.0	72	2 T25860	hypothetical prote
15	21	100.0	78	2 A63165	hypothetical prote
16	21	100.0	80	2 T11069	NADH2 dehydrogenas
17	21	100.0	85	2 H69191	hypothetical prote
18	21	100.0	89	2 S72598	sulfate permease T
19	21	100.0	90	2 A65037	hypothetical 9.9 k
20	21	100.0	90	2 C85905	hypothetical prote
21	21	100.0	90	2 E91060	hypothetical prote
22	21	100.0	97	2 S12958	tachykinin delta p
23	21	100.0	102	2 G72756	hypothetical prote
24	21	100.0	105	2 F72614	hypothetical prote
25	21	100.0	106	2 G81275	hypothetical prote
26	21	100.0	109	2 I52333	GI phase-specific
27	21	100.0	110	2 G69609	cytochrome-c oxida
28	21	100.0	112	1 SPRTA	substance P alpha
29	21	100.0	112	2 TS1238	scarecrow-like pro

#### ALIGNMENTS

##### RESULT 1

SPHO

substance P - horse

C:Species: Equus caballus (domestic horse)

C:Date: 23-Oct-1981 #sequence\_revision 23-Oct-1981 #text\_change 23-Aug-1996

C:Accession: A01558

R:Studer, R.O.; Trzeciak, A.; Lergier, W.

Helv. Chim. Acta 56, 860-866, 1973

A:Title: Isolierung und Aminosaeuresequenz von Substanz P aus Pferdedarm.

A:Reference number: A01558

A:Accession: A01558

A:Molecule type: protein

A:Residues: 1-11 <STU>

C:Superfamily: Substance P precursor

C:Keywords: amidated carboxyl end; hormone

F:Full/Modified site: amidated carboxyl end (Met) #status experimental

Query Match

Best Local Similarity 100.0%; Score 21; DB 1; Length 11;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4

Db 8 FGLM 11

##### RESULT 2

A60654

substance P - guinea pig

C:Species: Cavia porcellus (guinea pig)

C:Date: 14-May-1993 #sequence\_revision 27-Jun-1994 #text\_change 08-Dec-1995

C:Accession: A60654

R:Murphy, R.

Neuropeptides 14, 105-110, 1989

A:Title: Primary amino acid sequence of guinea-pig substance P.

A:Reference number: A60654; PMID:90044685; PMID:2478925

A:Accession: A60654

A:Molecule type: protein

A:Residues: 1-11 <MUR>

C:Superfamily: substance P precursor

C:Keywords: amidated carboxyl end; neuropeptide; tachykinin

F:Full/Modified site: amidated carboxyl end (Met) #status experimental

Query Match

Best Local Similarity 100.0%; Score 21; DB 1; Length 11;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4

Db 8 FGLM 11

substance P gamma  
tachykinin 1 precu  
hypothetical prote  
hypothetical prote  
NADH2 dehydrogenas  
hypothetical prote  
hypothetical prote  
cytochrome P450 CY  
Zn-finger containi  
protein ZK1240.6  
neurokinin 1 precu  
conserved hypothet  
substance P beta p  
neurokinin 1 precu  
tachykinin 1 precu  
neurokinin 1 precu

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
JN0023
substance P - chicken
C:Species: Gallus gallus (chicken)
C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 11-Jul-1997
C:Accession: JN0023
R:Conlon, J.M.; Katsoulis, S.; Schmidt, W.B.; Thim, L.
Regul. Pept. 20, 171-180, 1988
A>Title: [Arg3]substance P and neurokinin A from chicken small intestine.
A:Reference number: JN0023; MUID:88204263; PMID:2452461
A:Accession: JN0023
A:Molecule type: protein
A:Residues: 1-11 <CON>
C:Superfamily: unassigned animal peptides
C:Keywords: amidated carboxyl end; tachykinin
F:1/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 100.0%; Score 21; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4
Db 8 FGLM 11

RESULT 4
F60409
substance P-like peptide II - frog (Pseudophryne guentheri)
C:Species: Pseudophryne guentheri
C>Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 02-Sep-2000
C:Accession: F60409
R:Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.; Melchior
Peptides 11, 299-304, 1990
A>Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Austr
A:Reference number: A60409; MUID:90287814; PMID:2356157
A:Accession: F60409
A:Molecule type: protein
A:Residues: 1-11 <SIM>
C:Superfamily: unassigned animal peptides
C:Keywords: amidated carboxyl end; pyroglutamic acid
F:1/Modified site: pyroglutamate carboxylic acid (Gln) #status experimental
F:1/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 100.0%; Score 21; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4
Db 8 FGLM 11

RESULT 5
E60409
substance P-like peptide I - frog (Pseudophryne guentheri)
C:Species: Pseudophryne guentheri
C>Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 02-Sep-2000
C:Accession: E60409
R:Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.; Melchior
Peptides 11, 299-304, 1990
A>Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Austr
A:Reference number: A60409; MUID:90287814; PMID:2356157
A:Accession: E60409
A:Molecule type: protein
A:Residues: 1-11 <SIM>
C:Superfamily: unassigned animal peptides
C:Keywords: amidated carboxyl end; pyroglutamic acid
F:1/Modified site: pyroglutamate carboxylic acid (Gln) #status experimental
F:1/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 100.0%; Score 21; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4
Db 8 FGLM 11

RESULT 6
S23308
substance P - rainbow trout
C:Species: Oncorhynchus mykiss (rainbow trout)
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 18-Aug-2000
C:Accession: S23308
R:Jensen, J.; Conlon, J.M.
Eur. J. Biochem. 206, 659-664, 1992
A>Title: Substance P-related and neurokinin-A-related peptides from the brain of the cod
A:Reference number: S23186; MUID:92298992; PMID:1376687
A:Accession: S23308
A:Molecule type: protein
A:Residues: 1-11 <JEN>
A:Experimental source: brain
C:Function:
A:Description: may play a physiological role in the regulation of cardiovascular and gas
A>Note: substance P is derived by post-translational processing of preprotachykinin A
C:Superfamily: unassigned animal peptides
C:Keywords: neuropeptide; amidated carboxyl end; tachykinin
F:1/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 100.0%; Score 21; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4
Db 8 FGLM 11

RESULT 7
S33300
probable substance P - smaller spotted catehawk
C:Species: Scyllorhinus canicula (smaller spotted catehawk, smaller spotted dogfish)
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Mar-1999
C:Accession: S33300
R:Waugh, D.; Wang, Y.; Hazon, N.; Balmert, R.J.; Conlon, J.M.
Eur. J. Biochem. 214, 469-474, 1993
A>Title: Primary structures and biological activities of substance P-related peptides f
A:Reference number: S33300; MUID:93292508; PMID:7685693
A:Accession: S33300
A:Molecule type: protein
A:Residues: 1-11 <WAU>
A:Experimental source: brain
C:Function:
A:Description: may play a physiological role in the regulation of cardiovascular and ga
A>Note: substance P is derived by post-translational processing of preprotachykinin A
C:Keywords: amidated carboxyl end; neuropeptide; tachykinin
F:1/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 100.0%; Score 21; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4
Db 8 FGLM 11

RESULT 8
PS0332
phospholipase A2 (EC 3.1.1.4), sperm - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 31-Mar-2000
C:Accession: PS0332
R:Langlais, J.; Chafouleas, J.G.; Ingraham, R.; Vigneault, N.; Roberts, K.D.

```



Biochem. Biophys. Res. Commun. 182, 208-214, 1992  
 A:Title: The phospholipase A2 of human spermatozoa: purification and partial sequence.  
 A:Reference number: PS0332; MUID:92118015; PMID:1731781  
 A:Accession: PS0332  
 A:Molecule type: protein  
 A:Residues: 1-19 <LAN>  
 C:Keywords: carboxylic ester hydrolase

Query Match 100.0%; Score 21; DB 2; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 33;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4  
 ||||  
 DB 5 FGLM 8

## RESULT 9

hypothetical protein yrzK - Bacillus subtilis  
 C:Species: Bacillus subtilis  
 C:Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 15-Oct-1999  
 A:Accession: A69983  
 R:Kunze, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertea, C.; Bron, S.; Brouillet, S.; Bruschini, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chao, A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.; Nature 390, 249-256, 1997  
 A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallier, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parto, V.; Pohl, T.M.; Portetelle, Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A.; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror, Akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpsira, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.  
 A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.  
 A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.  
 A:Reference number: A69580; MUID:98044033; PMID:9384377  
 A:Accession: A69983  
 A>Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-56 <KUN>  
 A:Cross-references: GB:Z99118; GB:AL009126; NID:32635200; PIDN:CAB14716.1; PID:el184005;  
 A:Experimental source: strain 168  
 C:Genetics:  
 A:Gene: yrzK

Query Match 100.0%; Score 21; DB 2; Length 56;  
 Best Local Similarity 100.0%; Pred. No. 1e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4  
 ||||  
 DB 39 FGLM 42

## RESULT 10

JC2412  
 tachykinin gamma chain precursor - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 25-Feb-1995 #sequence\_revision 26-May-1995 #text\_change 17-Mar-1999  
 A:Accession: JC2412  
 R:Khan, I.; Collins, S.M.  
 Biochem. Biophys. Res. Commun. 202, 796-802, 1994  
 A:Title: Fourth isoform of preprotachykinin messenger RNA encoding for substance P in the rat.  
 A:Reference number: JC2411; MUID:94324969; PMID:7519424  
 A:Accession: JC2412  
 A:Molecule type: mRNA  
 A:Residues: 1-63 <KHA>  
 A:Superfamily: substance P precursor  
 C:Keywords: amidated carboxyl end  
 F:12-21/Product: substance P #status predicted <SUP>

Query Match 100.0%; Score 21; DB 2; Length 72;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## RESULT 13

JC5455  
 preprotachykinin-A gamma precursor - bovine  
 C:Species: Bos primigenius taurus (cattle)  
 C:Date: 10-Jul-1997 #sequence\_revision 29-Aug-1997 #text\_change 16-Jul-1999  
 C:Accession: JC5455; I45967

F:21/Modified site: amidated carboxyl end (Met) (amide in mature form from following gly  
 Query Match 100.0%; Score 21; DB 2; Length 63;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4  
 ||||  
 DB 18 FGLM 21

## RESULT 11

S04666  
 hypothetical protein 1 - Rhodospseudomonas blastica (fragment)  
 C:Species: Rhodospseudomonas blastica  
 C:Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 18-Jun-1993  
 A:Accession: S04666  
 R:Tybulewicz, V.L.J.; Falk, G.; Walker, J.E.  
 J. Mol. Biol. 179, 185-214, 1984  
 A:Title: Rhodospseudomonas blastica atp operon. Nucleotide sequence and transcription.  
 A:Reference number: S04666; MUID:85058188; PMID:6209404  
 A:Accession: S04666  
 A>Status: not compared with conceptual translation  
 A:Molecule type: DNA  
 A:Residues: 1-69 <TYB>

Query Match 100.0%; Score 21; DB 2; Length 69;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4  
 ||||  
 DB 18 FGLM 21

## RESULT 12

I62742  
 tachykinin A gamma chain precursor - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 16-Jul-1999  
 A:Accession: I62742; JC5453  
 R:Chiwakata, C.; Brackmann, B.; Hunt, N.; Davidoff, M.; Schulze, W.; Ivell, R.  
 Endocrinology 128, 2441-2448, 1991  
 A:Title: Tachykinin (substance-P) gene expression in Leydig cells of the human and mouse  
 A:Reference number: JC5450; MUID:91209287; PMID:1708336  
 A:Accession: I62742  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-72 <RES>  
 A:Cross-references: GB:M68909; NID:9200469; PIDN:AAA39970.1; PID:9554261  
 C:Comment: This protein contains two tachykinin peptide hormone substance-P which is inv  
 C:Genetics:

Query Match 100.0%; Score 21; DB 2; Length 72;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4  
 ||||  
 DB 30 FGLM 33

A;Cross-references: GB:AB008687; PIDN:AAL45739.1; PID:g17743471; GSPDB:GN00188  
A;Experimental source: strain C58 (Dupont)  
C;Genetics:  
A;Gene: Atu5047  
A;Genome: plasmid  
Query Match 100.0%; Score 21; DB 2; Length 78;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 FGLM 4  
Db 22 FGLM 25  
Search completed: August 25, 2004, 14:07:11  
Job time : 48 secs

R;Chiwakata, C.; Brackmann, B.; Hunt, N.; Davidoff, M.; Schulze, W.; Ivell, R.  
Endocrinology 128, 2441-2448, 1991  
A;Title: Tachykinin (substance-P) gene expression in Leydig cells of the human and mouse  
A;Reference number: JC5450; MUID:91209287; PMID:1708336  
A;Accession: JC5455  
A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-72 <CHI>  
A;Cross-references: GB:M68912; MID:g163593; PIDN:AAA30725.1; PID:g552336  
F;23-33/Product: substance-P #status predicted <STP>  
F;48-57/Product: neurokinin-A #status predicted <NKA>  
C;Genetics:  
A;Gene: PPT-A  
C;Superfamily: substance P precursor  
F;1-22/Domain: signal sequence #status predicted <SIG>  
F;23-33/Product: substance-P #status predicted <STP>  
F;48-57/Product: neurokinin-A #status predicted <NKA>  
Query Match 100.0%; Score 21; DB 2; Length 72;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 FGLM 4  
Db 30 FGLM 33

RESULT 14  
T25860  
hypothetical protein T04C9.3 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C;Accession: T25860  
R;Favella, A.  
submitted to the EMBL Data Library, December 1996  
A;Description: The sequence of C. elegans cosmid T04C9.  
A;Reference number: Z20101  
A;Accession: T25860  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-72 <FAV>  
A;Cross-references: EMBL:U80955; PIDN:AAE38101.1; GSPDB:GN00021; CESP:T04C9.3  
A;Experimental source: strain Bristol N2; clone T04C9  
C;Genetics:  
A;Gene: CESP:T04C9.3  
A;Map position: 3

Query Match 100.0%; Score 21; DB 2; Length 72;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGLM 4  
Db 24 FGLM 27

RESULT 15  
AB3165  
hypothetical protein Atu5047 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)  
C;Species: Agrobacterium tumefaciens  
C;Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 18-Nov-2002  
C;Accession: AE3165  
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.  
erage, G.; Gillet, W.; Grant, C.; Quentner, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell  
; Karp, P.; Romero, P.; Zhang, S.  
Science 294, 2317-2323, 2001  
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,  
ster, E.W.  
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.  
A;Reference number: AB2577; MUID:21608550; PMID:11743193  
A;Accession: AB3165  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-78 <KUR>

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OM protein - protein search, using sw model

Run on: August 25, 2004, 13:41:56 ; Search time 22 Seconds  
(without alignments)  
9.467 Million cell updates/sec

Title: US-10-053-669-2  
Perfect score: 21  
Sequence: 1 FGLM 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141691 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141691

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	21	100.0	11	TKN4_PSEGU	P42989 pseudophryn
2	21	100.0	11	TKN5_PSEGU	P42990 pseudophryn
3	21	100.0	11	TKNA_CHICK	P19850 gallus gall
4	21	100.0	11	TKNA_HORSE	P01290 equus cabal
5	21	100.0	11	TKNA_ONCMY	P28499 oncorynchu
6	21	100.0	11	TKNA_SCYCA	P41333 scyliorhinu
7	21	100.0	19	PA2S_HUMAN	P24606 homo sapien
8	21	100.0	56	YRZK_BACSU	O32040 bacillus su
9	21	100.0	69	Y010_TROWT	P59486 tropheryma
10	21	100.0	69	YAT1_RHOBL	P05443 rhodopseude
11	21	100.0	90	Y040_CORGL	P8mu99 corynebacte
12	21	100.0	90	YFTM_ECOLI	P46126 escherichia
13	21	100.0	95	MGBB_HUMAN	O75556 homo sapien
14	21	100.0	96	Y87A_HAEIN	O86229 haemophilus
15	21	100.0	110	COM4_BACSU	P24013 bacillus su
16	21	100.0	114	YE96_METUA	P41540 oryctolagus
17	21	100.0	115	TKN1_RABIT	O47429 brachiosco
18	21	100.0	117	NIJM_BRALA	P20366 homo sapien
19	21	100.0	129	TKN1_HUMAN	P01289 bos taurus
20	21	100.0	130	TKN1_BOVIN	Q60541 mesocricetu
21	21	100.0	130	TKN1_MESAU	P41539 mus musculu
22	21	100.0	130	TKN1_MOUSE	P06767 rattus norv
23	21	100.0	130	TKN1_RAT	P59832 klebsiella
24	21	100.0	131	LACY_KLEPN	Q918p6 gallus gall
25	21	100.0	132	OTOR_CHICK	P14528 escherichia
26	21	100.0	134	YQ9E_ECOLI	P14528 calyptogena
27	21	100.0	136	GLB2_CALSO	P02415 mycoplasma
28	21	100.0	137	RL16_MYCCA	Q9rn08 bacillus an
29	21	100.0	166	Y024_BACAN	Q95919 polypetrus
30	21	100.0	167	NI6M_POLOR	P00718 anser anser
31	21	100.0	185	LYG_ANSAN	P00717 cygnus atra
32	21	100.0	185	LYG_CYGAT	P00719 struthio ca
33	21	100.0	185	LYG_STRCA	

34 21 100.0 194 1 LSPA\_RICPR Q92dc4 rickettsia  
35 21 100.0 196 1 DCD\_WIGBR Q8d218 wigglsworth  
36 21 100.0 196 1 SPMA\_BACSU P35157 bacillus su  
37 21 100.0 200 1 Y933\_HELPJ Q92kt8 helicobacte  
38 21 100.0 200 1 Y933\_HELPJ Q25587 helicobacte  
39 21 100.0 201 1 LSPA\_RICPN Q92i62 rickettsia  
40 21 100.0 206 1 DCTM\_PARN Q56347 paracoccus  
41 21 100.0 207 1 COX3\_BACSU P24012 bacillus su  
42 21 100.0 210 1 MOBI\_SCHPO Q94360 schizosacch  
43 21 100.0 210 1 YD07\_HAEIN Q57320 haemophilus  
44 21 100.0 211 1 LYG\_CHICK P27042 gallus gall  
45 21 100.0 213 1 NQRD\_CHLCV Q823p4 chlamydomon

## ALIGNMENTS

RESULT 1  
TKN4\_PSEGU  
ID TKN4\_PSEGU STANDARD; PRT; 11 AA.  
AC P42989;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Substance P-like peptide I (PG-SPI).  
OS Pseudophryne guentheri (Guenther's toadlet).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Myobatrachidae;  
OC Myobatrachinae; Pseudophryne.  
OX NCBI\_TaxID=30349;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Skin secretion;  
RX MEDLINE=90287814; PubMed=2356157;  
RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,  
RA Roberts J.D., Melchiorri P., Espaner V.,  
RT "Six novel tachykinin- and bombesin-related peptides from the skin of  
RT the Australian frog Pseudophryne guntheri.";  
RL Peptides 11:299-304(1990).  
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
CC evoke behavioral responses, are potent vasodilators and  
CC secretagogues, and contract (directly or indirectly) many smooth  
CC muscles.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Skin.  
CC -!- SIMILARITY: Belongs to the tachykinin family.  
CC PIR; E60409; E60409.  
DR InterPro; IPR002040; Tachy Neurokinin.  
DR InterPro; IPR008215; Tachykinin.  
DR Pfam; PF02202; Tachykinin; 1.  
DR SMART; SM00203; TK; 1.  
DR PROSITE; PS00267; TACHYKININ; 1.  
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;  
KW Pyrrolidone carboxylic acid; Tachykinin; Neuropeptide; Amidation;  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT MOD\_RES 11 11 AMIDATION.  
SQ SEQUENCE 11 AA; 1294 MW; 3A247C2CC9C81AB7 CRC64;  
Query Match 100.0%; Score 21; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FGLM 4  
Db 8 FGLM 11  
RESULT 2  
TKN5\_PSEGU  
ID TKN5\_PSEGU STANDARD; PRT; 11 AA.  
AC P42990;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT	10-OCT-2003 (Rel. 42, Last annotation update)
DE	Substance P-like peptide II (pg-SP11).
OS	Pseudophryne guentheri (Guenther's toadlet).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Amphibia; Batrachia; Anura; Neobatrachia; Hylaidea; Myobatrachidae;
OC	Myobatrachinae; Pseudophryne.
OX	NCBI_TaxID=30349;
RN	[1]
RP	SEQUENCE.
RC	TISSUE=Skin secretion;
RX	MEDLINE=90287814; PubMed=2356157;
RA	Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
RA	Roberts J.D., Melchiorri P., Espamer V.;
RT	"Six novel tachykinin- and bombesin-related peptides from the skin of
RT	the Australian frog pseudophryne guentheri.";
RL	Peptides 11:299-304(1990).
CC	-1- FUNCTION: Tachykinins are active peptides which excite neurons,
CC	evoked behavioral responses, are potent vasodilators and
CC	secretagogues, and contract (directly or indirectly) many smooth
CC	muscles.
CC	-1- SUBCELLULAR LOCATION: Secreted.
CC	-1- TISSUE SPECIFICITY: Skin.
CC	-1- SIMILARITY: Belongs to the tachykinin family.
DR	PIR; F60409; F60409.
DR	InterPro; IPR002040; Tachy Neurokinin.
DR	InterPro; IPR008215; Tachykinin.
DR	Pfam; PF02202; Tachykinin; 1.
DR	SMART; SM00203; TK; 1.
DR	PROSITE; PS00267; TACHYKININ; 1.
KW	Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
KW	Pyroglutamate carboxylic acid.
FT	MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT	MOD RES 11 11 AMIDATION.
SQ	SEQUENCE 11 AA; 1293 MW; 3A247C2CC9CB1457 CRC64;
Query Match 100.0%; Score 21; DB 1; Length 11;	
Best Local Similarity 100.0%; Pred. No. 16;	
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps	
QY	1 FGLM 4
DB	8 FGLM 11
RESULT 3	
TKNA_CHKCK	
ID	TKNA_CHKCK STANDARD; PRT; 11 AA.
AC	P19850;
DT	01-FEB-1991 (Rel. 17, Created)
DT	01-FEB-1991 (Rel. 17, Last sequence update)
DT	10-OCT-2003 (Rel. 42, Last annotation update)
DE	Substance P.
OS	Gallus gallus (Chicken).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC	Gallus.
OX	NCBI_TaxID=9031;
RN	[1]
RP	SEQUENCE.
RC	TISSUE=Intestine;
RX	MEDLINE=89204263; PubMed=2452461;
RA	Conlon J.M., Katsoulis S., Schmidt W.E., Thim L.;
RT	"[Arg3]substance P and neurokinin A from chicken small intestine.";
RL	Regul. Pept. 20:171-180(1988).
CC	-1- FUNCTION: Tachykinins are active peptides which excite neurons,
CC	evoked behavioral responses, are potent vasodilators and
CC	secretagogues, and contract (directly or indirectly) many smooth
CC	muscles.
CC	-1- SUBCELLULAR LOCATION: Secreted.
CC	-1- SIMILARITY: Belongs to the tachykinin family.
DR	PIR; JN0023; JN0023.
DR	InterPro; IPR002040; Tachy Neurokinin.
DR	Pfam; PF02202; Tachykinin; 1.

DT 01-DEC-1992 (Rel. 24, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Substance P.  
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
OX Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
NCBI\_TaxID=8022;  
RN [1]  
RP SEQUENCE  
RC TISSUE=Brain;  
RX MEDLINE=92298992; PubMed=1376687;  
RA Jensen J., Conlon J.M.;  
RT "Substance-P-related and neurokinin-A-related peptides from the brain  
of the cod and trout."  
RL Eur. J. Biochem. 206:659-664(1992).  
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
CC evoke behavioral responses, are potent vasodilators and  
CC secretagogues, and contract (directly or indirectly) many smooth  
CC muscles.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to the tachykinin family.  
DR PIR; S23308; S23308.  
DR InterPro; IPR002040; Tachy Neurokinin.  
DR Pfam; PF02202; Tachykinin.  
DR SMART; SM00203; TK; 1.  
DR PROSITE; PS00267; TACHYKININ; 1.  
KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.  
FT MOD\_RES 11  
FT MOD\_RES 11 AMIDATION (BY SIMILARITY).  
SQ SEQUENCE 11 AA; 1358 MW; 214860DEC9D6D1F7 CRC64;  
Query Match 100.0%; Score 21; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FGLM 4  
DB 8 FGLM 11  
RESULT 6  
ID TKNA SCYCA STANDARD; PRT; 11 AA.  
AC P41333;  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Substance P.  
OS Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;  
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;  
OC Scyliorhinidae; Scyliorhinus.  
OX NCBI\_TaxID=7830;  
RN [1]  
RP SEQUENCE  
RC TISSUE=Brain;  
RX MEDLINE=93292508; PubMed=7685693;  
RA Waugh D., Wang Y., Hazen N., Balmert R.J., Conlon J.M.;  
RT "Primary structures and biological activities of substance-P-related  
peptides from the brain of the dogfish, Scyliorhinus canicula."  
RL Eur. J. Biochem. 214:469-474(1993).  
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
CC evoke behavioral responses, are potent vasodilators and  
CC secretagogues, and contract (directly or indirectly) many smooth  
CC muscles.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to the tachykinin family.  
DR PIR; S33300; S33300.  
DR InterPro; IPR002040; Tachy Neurokinin.  
DR PROSITE; PS00267; TACHYKININ; 1.  
KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.  
FT MOD\_RES 11  
FT MOD\_RES 11 AMIDATION.

SQ SEQUENCE 11 AA; 1278 MW; 214860DEC9D6D867 CRC64;  
Query Match 100.0%; Score 21; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FGLM 4  
DB 8 FGLM 11  
RESULT 7  
ID PA2S HUMAN STANDARD; PRT; 19 AA.  
AC F24606;  
DT 01-MAR-1992 (Rel. 21, Created)  
DT 01-MAR-1992 (Rel. 21, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Phospholipase A2, spermatozoa (EC 3.1.1.4) (Phosphatidylcholine  
2-acylhydrolase) (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE  
RC TISSUE=Semen;  
RX MEDLINE=92118015; PubMed=1731781;  
RA Langlais J., Chafouleas J.G., Ingraham R., Vigneault N., Roberts K.D.;  
RT "The phospholipase A2 of human spermatozoa; purification and partial  
sequence."  
RL Biochem. Biophys. Res. Commun. 182:208-214(1992).  
CC -!- FUNCTION: Believed to play a key role in the acrosome reaction via  
CC the enzymatic hydrolysis of unsaturated fatty acids linked to  
CC membrane phospholipids overlying the acrosome of mammalian  
CC spermatozoa.  
CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-  
CC acylglycerophosphocholine + a fatty acid anion.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to the phospholipase A2 family.  
DR PIR; PS0332; PS0332.  
DR GO; GO:004623; F:phospholipase A2 activity; NAS.  
DR GO; GO:0007340; P:acrosome reaction; NAS.  
DR InterPro; IPR001211; PhospholipaseA2.  
DR PROSITE; PS00118; PA2\_HIS; PARTIAL.  
DR PROSITE; PS00119; PA2\_ASP; PARTIAL.  
KW Hydrolase; Lipid degradation.  
FT NON\_TER 19  
FT NON\_TER 19  
SQ SEQUENCE 19 AA; 2233 MW; 88CE016056C3BEBB CRC64;  
Query Match 100.0%; Score 21; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FGLM 4  
DB 5 FGLM 8  
RESULT 8  
ID YRZK\_BACSU STANDARD; PRT; 56 AA.  
AC O32040;  
DT 10-OCT-2003 (Rel. 42, Created)  
DT 10-OCT-2003 (Rel. 42, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Hypothetical protein yrzK.  
GN YRZK OR BSU27570.  
OS Bacillus subtilis.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=1423;  
RN [1]  
RP SEQUENCE FROM N.A.

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RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borcherdt S.,
RA Borriess R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Chouliet S., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.F.,
RA Entian K.D., Errington J., Fabret C., Ferraci A., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Chim S.Y., Glaeser P., Goffeau A., Goughly E.J., Grandi G.,
RA Guisepi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaiber-Blandhard M., Klein C.,
RA Kobayashi Y., Koester P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Maue C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Riva C., Roche E., Roche B., Rose M., Sadale Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpestra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambuit R., Wedler E., Wedler H., Weitzenegger T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,
RA "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis."
RT Nature 390:249-256 (1997).
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CC -----
CC EMBL; Z99118; CAB14716.1; -.
DR PIR; A69983; A69983.
DR Subtilist; BG13820; YrzK.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 56 AA; 6325 MW; DD489749F1C2200D CRC64;

Query Match 100.0%; Score 21; DB 1; Length 56;
Best Local Similarity 100.0%; Pred. No. 70; Mismatches 0; Gaps 0;
Matches 4; Conservative 0; Indels 0;

Qy 1 FGLM 4
Db 39 FGLM 42

RESULT 9
Y010 TROWT
ID Y010 TROWT STANDARD; PRT; 69 AA.
AC PS9456;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypothetical UPF0233 membrane protein TW010/TW010.
GN TW010 OR TW010.
OS Tropheryma whipplei (strain Twist) (Whipple's bacillus), and
OS Tropheryma whipplei (strain TW08/27) (Whipple's bacillus).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Micrococcales; Cellulomonadaceae; Tropheryma.
OX NCBI_TaxID=203267, 218496;
RN [1]
RP SEQUENCE FROM N.A.

STRAIN=Twist / Genotype 2A;
MEDLINE=22784088; PubMed=12902375;
RA Raoult D., Ogata H., Audic S., Robert C., Suhr K., Drancourt M.,
RA Claverie J.-M.;
RT "Tropheryma whipplei Twist: a human pathogenic Actinobacteria with a
RL reduced genome."
RN Genome Res. 13:1800-1809 (2003).
RP SEQUENCE FROM N.A.
RX STRAIN=TW08/27;
RX MEDLINE=22495039; PubMed=12606174;
RA Bentley S.D., Mawald M., Murphy L.D., Pallen M.J., Yeats C.A.,
RA Dover L.G., Norbertczak H.T., Besta G.S., Quail M.A., Harris D.E.,
RA von Herbay A., Goble A., Rutter S., Squares R., Squares S.,
RA Barrell B.G., Parkhill J., Rellman D.A.;
RA "Sequencing and analysis of the genome of the Whipple's disease
RT bacterium Tropheryma whipplei."
RL Lancet 361:637-644 (2003).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: Belongs to the UPF0233 family.
CC -----
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CC -----
CC EMBL; AE016850; AAC44107.1; -.
DR EMBL; BX251410; CAD66702.1; -.
DR HAMAP; MF 00631; -; 1.
KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 14 34 POTENTIAL.
FT TRANSMEM 45 65 POTENTIAL.
SQ SEQUENCE 69 AA; 7723 MW; 3C83E5B3F154DD24 CRC64;

Query Match 100.0%; Score 21; DB 1; Length 69;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGLM 4
Db 21 FGLM 24

RESULT 10
YAT1 RHOB
ID YAT1 RHOB STANDARD; PRT; 69 AA.
AC P05443;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 01-NOV-1988 (Rel. 09, Last annotation update)
DE ATP synthase subunits region ORF 1 (Fragment).
OS Rhodopsedomonas blastica.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
OC Rhodobacteraceae; Rhodobacter.
OX NCBI_TaxID=1075;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85058188; PubMed=6209404;
RA Tybulewicz V.L.J., Falk G., Walker J.E.;
RT "Rhodopsedomonas blastica atp operon. Nucleotide sequence and
RT transcription."
RN J. Mol. Biol. 179:185-214 (1984).
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CC -----
DR EMBL; Z00018; CAA77307.1; --
DR PIR; S04666; S04666.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 69 AA; 7471 MW; 574EB0B6F8529ED9 CRC64;

Query Match 100.0%; Score 21; DB 1; Length 69;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4
DB 18 FGLM 21

RESULT 11
Y040 CORGL STANDARD; PRT; 90 AA.
AC Q8NU99;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypothetical UPF0233 membrane protein Cg10040.
GN Cg10040.
OS Corynebacterium glutamicum (Brevibacterium flavum).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=1718;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
RA Nakagawa S.;
RT "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: Belongs to the UPF0233 family.
CC
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CC -----
DR EMBL; AP005274; BAB97433.1; --
DR HAMAP; MF_00631; -- 1.
KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 38 58
FT TRANSMEM 67 87
SQ SEQUENCE 90 AA; 9950 MW; F3E9B657A4089E5D CRC64;

Query Match 100.0%; Score 21; DB 1; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4
DB 76 FGLM 79

RESULT 12
YFIM ECOLI
ID YFIM ECOLI STANDARD; PRT; 90 AA.
AC P46126;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein yfim.
GN YFIM OR B2586.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

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OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97349980; PubMed=9205837;
RA Yamamoto Y., Aiba H., Baba T., Hayashi K., Inada T., Isono K.,
RA Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N.,
RA Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nishimoto H.,
RA Oshima T., Oyama S., Saito N., Sampei G., Satoh Y., Sivasubram S.,
RA Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C.,
RA Yamagata S., Horiuchi T.;
RT "Construction of a contiguous 874-kb sequence of the Escherichia coli
RT - K12 genome corresponding to 50.0-68.8 min on the linkage map and
RT analysis of its sequence features.";
RL DNA Res. 4:91-113(1997).
RN [3]
RP SEQUENCE OF 1-53 FROM N.A.
RX MEDLINE=91161632; PubMed=2002065;
RA Dechavigny A., Heacock P.N., Dowhan W.;
RT "Sequence and inactivation of the pss gene of Escherichia coli.
RT Phosphatidylethanolamine may not be essential for cell viability.";
RL J. Biol. Chem. 266:5323-5332(1991).
RN [4]
RP SEQUENCE OF 23-90 FROM N.A.
RX STRAIN=K12;
RX MEDLINE=90368520; PubMed=2118499;
RA Seol W., Shatkin A.J.;
RT "A new gene located between pss and rrrG on the Escherichia coli
RT chromosome.";
RL J. Bacteriol. 172:4745-4745(1990).
RN [5]
RP IDENTIFICATION
RX MEDLINE=96032851; PubMed=7567469;
RA Borodovsky M., McIninch J., Koonin E.V., Rudd K.E., Medigue C.,
RA Danchin A.;
RT "Detection of new genes in a bacterial genome using Markov models for
RT three gene classes.";
RL Nucleic Acids Res. 23:3554-3562(1995).
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CC -----
DR EMBL; AE000345; AAC75639.1; --
DR EMBL; D90886; BAAL6471.1; --
DR EMBL; D90887; BAAL6471.1; --
DR EMBL; M58699; -- NOT ANNOTATED CDS.
DR EMBL; X75467; -- NOT ANNOTATED CDS.
DR EMBL; X53027; -- NOT ANNOTATED CDS.
DR PIR; A65037; A65037.
DR EcoGene; EG12857; yfim.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 90 AA; 9931 MW; 31E717CCECA6CEB14 CRC64;

Query Match 100.0%; Score 21; DB 1; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 FGLM 4
Db      42 FGLM 45

RESULT 13
MGBB HUMAN
ID MGBB HUMAN STANDARD; PRT; 95 AA.
AC O75556;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Mammaglobin B precursor (Mammaglobin 2) (Lipophilin C) (Lacryglobin)
DE (Secretoglobulin family 2A member 1).
GS SCGB2A1 OR MGB2 OR UGB3 OR LIPHC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99026127; PubMed=9806831;
RA Becker R.M., Darrow C., Zimonjic D.B., Popescu N.C., Watson M.A.,
RA Fleming T.P.;
RT Identification of mammaglobin B, a novel member of the uteroglobin
RT gene family."
RL Genomics 54:70-78(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99167354; PubMed=10066439;
RA Zhao C., Nguyen T., Yusifov T., Glasgow B.J., Lehrer R.I.;
RT "Lipophilins: human peptides homologous to rat prostatein.";
RL Biochem. Biophys. Res. Commun. 256:147-155(1999).
RN [3]
RP SEQUENCE OF 19-85.
RC TISSUE=Tears;
RX MEDLINE=98163342; PubMed=9504814;
RA Molloy M.P., Bolis S., Herbert B.R., Ou K., Tyler M.I., van Dyk D.D.,
RA Willcox M.D., Gootley A.A., Williams K.L., Morris C.A., Walsh B.J.;
RT "Establishment of the human reflex tear two-dimensional polyacrylamide
RT gel electrophoresis reference map: new proteins of potential
RT diagnostic value."
RL Electrophoresis 18:2811-2815(1997).
RN [4]
RP SEQUENCE OF 19-46 AND 60-78, AND MASS SPECTROMETRY.
RC TISSUE=Tears;
RX MEDLINE=98385871; PubMed=9720917;
RA Lehrer R.I., Xu G., Abduragimov A., Dinh N.N., Qu X.-D., Martin D.,
RA Glasgow B.J.;
RT "Lipophilin, a novel heterodimeric protein of human tears.";
RL FEBS Lett. 432:163-167(1998).
CC -1- FUNCTION: MAY BIND ANDROGENS AND OTHER STEROIDS, MAY ALSO BIND
CC ESTRAMUSTINE, A CHEMOTHERAPEUTIC AGENT USED FOR PROSTATE CANCER.
CC MAY BE UNDER TRANSCRIPTIONAL REGULATION OF STEROID HORMONES.
CC -1- SUBUNIT: HETERODIMER OF A LIPOPHILIN A AND A LIPOPHILIN C
CC (MAMMAGLOBIN B) MONOMER ASSOCIATED HEAD TO HEAD.
CC -1- TISSUE SPECIFICITY: Expressed in thymus, trachea, kidney, steroid
CC responsive tissues (prostate, testis, uterus, breast and ovary)
CC and salivary gland.
CC -1- MASS SPECTROMETRY: MW=8854.94; METHOD=Electrospray; RANGE=19-95.
CC -1- SIMILARITY: Belongs to the uteroglobin family. Lipophilin
CC subfamily.
CC
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CC
CC EMBL; U32769; AAC22539.1; -
CC TIGR; H10870.1; -
CC KW Hypothetical protein; Transmembrane; Complete proteome.
CC FT TRANSMEM 27 47 POTENTIAL.
CC EMBL; AJ224173; CAA11865.1; -
CC FT TRANSMEM 50 70 POTENTIAL.

Genew; HGNC:7051; SCGB2A1.
MIM; 604398; -.
GO; GO:0005497; F:androgen binding; NAS.
InterPro; IPR003627; Mambg/prostatn.
InterPro; IPR000329; Uterogloblin_subf.
InterPro; IPR006038; Uterogloblin_supf.
Pfam; PF01099; Uterogloblin; 1.
ProDom; PD029354; Mambg/prostatn; 1.
PROSITE; PS00403; UTEROGLOBLIN_1; FALSE_NEG.
PROSITE; PS00404; UTEROGLOBLIN_2; FALSE_NEG.
Signal; Glycoprotein.
KW SIGNAL 1 18
FT CHAIN 19 95 MAMMAGLOBIN B.
FT CARBOHYD 68 68 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 95 AA; 10884 MW; 0719738289F89F8D CRC64;

Query Match 100.0%; Score 21; DB 1; Length 95;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FGLM 4
Db      77 FGLM 80

RESULT 14
Y87A HAEIN
ID Y87A HAEIN STANDARD; PRT; 96 AA.
AC O86229;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein HI0870.1.
GN HI0870.1.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Rd / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.D., Geoghagen N.S.W.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
RT Rd.";
RL Science 269:496-512(1995).
RN [2]
RP IDENTIFICATION.
RA White O., Clayton R.A., Kerlavage A.R., Fleischmann R.D., Peterson J.,
RA Hickey E., Dodson R., Gwinn M.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
CC
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CC
CC EMBL; U32769; AAC22539.1; -
CC TIGR; H10870.1; -
CC KW Hypothetical protein; Transmembrane; Complete proteome.
CC FT TRANSMEM 27 47 POTENTIAL.
CC EMBL; AJ224173; CAA11865.1; -
CC FT TRANSMEM 50 70 POTENTIAL.

```



SQ SEQUENCE 96 AA; 11429 MW; 1A0FF09659E9E11150 CRC64;  
 Query Match 100.0%; Score 21; DB 1; Length 96;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4  
 Db 13 FGLM 16

RESULT 15  
 COX4\_BACSU STANDARD; PRT; 110 AA.  
 AC P24013;  
 DT 01-MAR-1992 (Rel. 21, Created)  
 DT 01-MAR-1992 (Rel. 21, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Cytochrome c oxidase polypeptide IVB (EC 1.9.3.1) (Cytochrome aa3  
 subunit 4B) (Caa-3605 subunit 4B).  
 GN CTAF OR BSU14920.  
 OS Bacillus subtilis.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1423;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=168;  
 RX MEDLINE=91146590; PubMed=1847686;  
 RA Saraste M., Metsö T., Nakari T., Jalli T., Lauraeus M.,  
 RA van der Oost J.;  
 RT "The Bacillus subtilis cytochrome-c oxidase. Variations on a  
 conserved protein theme."  
 RL Eur. J. Biochem. 195:517-525(1991).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=168;  
 RX MEDLINE=98044033; PubMed=9384377;  
 RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,  
 RA Azevedo V., Bertero M.G., Bessières P., Bolotin A., Borchert S.,  
 RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,  
 RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,  
 RA Choi S.K., Codani J.J., Conerton I.F., Cummings N.J., Daniel R.A.,  
 RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,  
 RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,  
 RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,  
 RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,  
 RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,  
 RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,  
 RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,  
 RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,  
 RA Kurita K., Lapidus A., Iardinois S., Lauber J., Lazarevic V.,  
 RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,  
 RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,  
 RA Neone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,  
 RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,  
 RA Prescean E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,  
 RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,  
 RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,  
 RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,  
 RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,  
 RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,  
 RA Tosato V., Uchiyama S., Vandenbol M., Vannier P., Vassarotti A.,  
 RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,  
 RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,  
 RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.;  
 RT "The complete genome sequence of the Gram-positive bacterium Bacillus  
 subtilis."

RL Nature 390:249-256(1997).  
 CC -1- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) = 4 ferricytochrome  
 c + 2 H(2)O.  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. CONTAINS 3  
 CC POTENTIAL TRANSMEMBRANE DOMAINS.  
 CC -----  
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 CC -----  
 DR EMBL; X54140; CAA38079.1; -;  
 DR EMBL; Z98682; CAB11345.1; -;  
 DR EMBL; Z99111; CAB13365.1; -;  
 DR PIR; G69609; G69609;  
 DR Subtilist; BG10218; ctaF.  
 DR InterPro; IPR005171; COX4\_pro.  
 DR Pfam; PF03626; COX4\_pro; 1.  
 KW Oxidoreductase; Transmembrane; Complete proteome.  
 SQ SEQUENCE 110 AA; 12620 MW; 1142CF36A63C3AF9 CRC64;

Query Match 100.0%; Score 21; DB 1; Length 110;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4  
 Db 32 FGLM 35

Search completed: August 25, 2004, 14:06:19  
 Job time : 24 secs

blank sheet

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 25, 2004, 13:59:47 ; Search time 121 Seconds

(without alignments)  
10.430 Million cell updates/sec

Title: US-10-053-669-2

Perfect score: 21

Sequence: 1 FGLM 4

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL\_25:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phase:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_virus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archaea:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	21	100.0	19	10 Q9S8E2	Q9S8E2 spinacia ol
2	21	100.0	41	16 Q7UFM5	Q7UFM5 rhodospirell
3	21	100.0	46	16 Q87RM6	Q87RM6 vibrio para
4	21	100.0	53	5 Q9TYI4	Q9TYI4 caenorhabdi
5	21	100.0	55	5 O17544	O17544 caenorhabdi
6	21	100.0	55	5 O44360	O44360 ceratitidis c
7	21	100.0	58	16 Q8EMM4	Q8EMM4 oceanobacil
8	21	100.0	63	6 Q9GNL1	Q9GNL1 macaca fasc
9	21	100.0	63	16 Q82X04	Q82X04 nitrosomona
10	21	100.0	64	5 Q86H30	Q86H30 dictyosteli
11	21	100.0	67	10 Q8GTG4	Q8GTG4 lycopersico
12	21	100.0	67	17 Q8TLV1	Q8TLV1 methanosarc
13	21	100.0	68	2 Q05625	Q05625 staphylococ
14	21	100.0	68	2 Q50886	Q50886 myxococcus
15	21	100.0	72	4 Q9Y494	Q9Y494 homo sapien
16	21	100.0	72	5 Q9GP92	Q9GP92 caenorhabdi

17	21	100.0	72	16 Q8CSF7	Q8CSF7 staphylococ
18	21	100.0	74	4 Q81WZ7	Q81WZ7 homo sapien
19	21	100.0	76	4 Q86UU6	Q86UU6 homo sapien
20	21	100.0	78	2 Q8VV82	Q8VV82 colwellia m
21	21	100.0	78	16 Q8UKQ3	Q8UKQ3 agrobacteri
22	21	100.0	79	2 Q8KZ14	Q8KZ14 uncultured
23	21	100.0	79	8 Q8HN49	Q8HN49 brugia mala
24	21	100.0	80	8 Q47577	Q47577 onchocerca
25	21	100.0	80	16 Q98N11	Q98N11 rhizobium l
26	21	100.0	81	16 Q8XN79	Q8XN79 clostridium
27	21	100.0	81	16 Q8D627	Q8D627 vibrio vuln
28	21	100.0	84	12 Q95927	Q95927 carnation m
29	21	100.0	84	16 Q8E405	Q8E405 streptococ
30	21	100.0	85	17 Q26173	Q26173 methanobact
31	21	100.0	87	4 Q86UU7	Q86UU7 homo sapien
32	21	100.0	88	9 Q8LT78	Q8LT78 vibriophage
33	21	100.0	88	16 Q7UGH0	Q7UGH0 rhodospirell
34	21	100.0	89	2 Q49761	Q49761 mycobacteri
35	21	100.0	90	9 Q8H9X0	Q8H9X0 pseudomonas
36	21	100.0	90	10 Q94UM6	Q94UM6 oryza sativ
37	21	100.0	90	16 Q8X9F4	Q8X9F4 escherichia
38	21	100.0	90	16 Q7UBW7	Q7UBW7 shigella fl
39	21	100.0	93	2 Q9Z9I6	Q9Z9I6 escherichia
40	21	100.0	96	4 Q86UU8	Q86UU8 homo sapien
41	21	100.0	97	2 Q68974	Q68974 synchococ
42	21	100.0	97	11 Q920K2	Q920K2 cavia porce
43	21	100.0	99	16 Q9RD07	Q9RD07 streptomyce
44	21	100.0	102	17 Q9YG57	Q9YG57 aeropyrum p
45	21	100.0	104	16 Q92MW6	Q92MW6 rhizobium m

#### ALIGNMENTS

RESULT 1

Q9S8E2 PRELIMINARY; PRT; 19 AA.

AC Q9S8E2; 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)

DE 6.1 kDa nuclear-encoded photosystem II reaction center subunit (Fragment).

OS Spinacia oleracea (Spinach).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; OC Caryophyllales; Amaranthaceae; Spinacia.

OX NCBI\_TaxID=3562;

RN [1]\_TaxID=3562;

RP SEQUENCE.

RA MEDLINE=95340559; PubMed=7615565;

RA Irrgang K.D., Shi L.X., Funk C., Schroder W.P.;

RT "A nuclear-encoded subunit of the photosystem II reaction center.";

RL J. Biol. Chem. 270:17588-17593(1995).

SQ SEQUENCE 19 AA; 2067 MW; 547B56337B5719E7 CRC64;

Query Match Best Local Similarity 100.0%; Score 21; DB 10; Length 19;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGLM 4

Db 15 FGLM 18

RESULT 2

Q7UFM5 PRELIMINARY; PRT; 41 AA.

ID Q7UFM5; 01-OCT-2003 (TREMBLrel. 25, Created)

DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)

DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DE Hypothetical protein.

GN RB473.  
OS Rhodopirellula baltica.  
OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;  
OC Planctomycetaceae; Pirellula.  
OX NCBI\_TaxID=117;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=1;  
RX MEDLINE=22735913; PubMed=12835416;  
RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,  
RA Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,  
RA Schleesner H., Amann R., Reinhardt R.,  
RT "Complete genome sequence of the marine planctomycete Pirellula sp.  
RT strain 1.";  
RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303 (2003).  
RL EMBL; BX294147; CAD78657.1; -.  
RW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 41 AA; 4390 MW; 50080409436EC192 CRC64;  
  
Query Match 100.0%; Score 21; DB 16; Length 41;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 FGLM 4  
Db 4 FGLM 7  
  
RESULT 3  
Q87RM6 PRELIMINARY; PRT; 46 AA.  
AC Q87RM6  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Conserved hypothetical protein.  
GN VP0752.  
OS Vibrio parahaemolyticus.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;  
OC Vibrionaceae; Vibrio.  
OX NCBI\_TaxID=670;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=RIMD 2210633 / Serotype O3:K6;  
RX MEDLINE=22508454; PubMed=12620739;  
RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,  
RA Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,  
RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;  
RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism  
RT distinct from that of V. cholerae.";  
RL Lancet 361:743-749 (2003).  
RL EMBL; AP005075; BAC59015.1; -.  
RW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 46 AA; 5225 MW; 6413FC3DF8186097 CRC64;  
  
Query Match 100.0%; Score 21; DB 16; Length 46;  
Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 FGLM 4  
Db 25 FGLM 28  
  
RESULT 4  
Q9TYI4 PRELIMINARY; PRT; 53 AA.  
AC Q9TYI4  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Protein tyrosine kinase (EC 2.7.1.112) (Fragment).  
GN CEHD-17.

OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
OC Rhabditidae; Peloderinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Oates A.C., Wilks A.F.;  
RT "How many PTKs to organise a worm?";  
RL The Worm Breeders Gazette 14:87-87(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Oates A.C., Wollberg P., Achen M.G., Wilks A.F.;  
RT "Sampling the Genomic Pool of Protein Tyrosine Kinase Genes using the  
RT Polymerase Chain Reaction with Genomic DNA.";  
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ002903; CAA05738.1; -.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.  
DR GO; GO:0016740; F:transferase activity; IEA.  
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
DR InterPro; IPR000719; Prot\_kinase.  
DR ProDom; PD000001; Prot\_kinase; 1.  
KW Kinase; Transferase.  
FT NON\_TER 1  
FT NON\_TER 53  
SQ SEQUENCE 53 AA; 6207 MW; 2A352DE56CF2BCF6 CRC64;  
  
Query Match 100.0%; Score 21; DB 5; Length 53;  
Best Local Similarity 100.0%; Pred. No. 4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 FGLM 4  
Db 14 FGLM 17  
  
RESULT 5  
O17544 PRELIMINARY; PRT; 55 AA.  
AC O17544  
DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Protein tyrosine kinase (EC 2.7.1.112) (Fragment).  
GN CEHD-20.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
OC Rhabditidae; Peloderinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Oates A.C., Wilks A.F.;  
RT "How many PTKs to organise a worm?";  
RL The Worm Breeders Gazette 14:87-87(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Oates A.C., Wollberg P., Achen M.G., Wilks A.F.;  
RT "Sampling the Genomic Pool of Protein Tyrosine Kinase Genes using the  
RT Polymerase Chain Reaction with Genomic DNA.";  
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ002904; CAA05739.1; -.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.  
DR GO; GO:0016740; F:transferase activity; IEA.  
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
DR InterPro; IPR000719; Prot\_kinase.  
DR Pfam; PF00069; pkinase; 1.  
DR ProDom; PD000001; Prot\_kinase; 1.  
DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.  
KW ATP-binding; Kinase; Transferase.  
FT NON\_TER 1  
FT NON\_TER 55  
SQ SEQUENCE 55 AA; 6491 MW; 5EEEC59354164E7 CRC64;

Query Match 100.0%; Score 21; DB 5; Length 55;  
Best Local Similarity 100.0%; Pred. No. 4.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4  
DB 15 FGLM 18

RESULT 6  
O44360  
ID O44360 PRELIMINARY; PRT; 55 AA.  
AC O44360;  
DT 01-JUN-1998 (TrEMBLrel. 06, Created)  
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Cytochrome P450 monooxygenase (DUI54CC) (Fragment).  
GN CYP6A11.  
OS Ceratitis capitata (Mediterranean fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Tephritoidea; Tephritidae; Ceratitis.  
OX NCBI\_TaxID=7213;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Danielson P.B., Foster J.L.M., Cooper S.K., Fogleman J.C.;  
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.  
CC -!- CATALYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) = ROH +  
CC OXIDIZED FLAVOPROTEIN + H(2)O.  
CC -!- SUBCELLULAR LOCATION: MEMBRANE-BOUND. ENDOPLASMIC RETICULUM (BY  
CC SIMILARITY).  
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.  
DR EMBL; AF028002; BAB94119.1; --  
DR GO; GO:0005783; C:cytoplasmic reticulum; IEA.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0005792; C:microsome; IEA.  
DR GO; GO:0004497; F:monooxygenase activity; IEA.  
DR GO; GO:0006118; P:electron transport; IEA.  
DR InterPro; IPR001128; Cytochrome\_P450.  
KW Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;  
KW Microsome; Endoplasmic reticulum.  
FT NON\_TER 1  
SQ SEQUENCE 55 AA; 6332 MW; D182B26FF3850513 CRC64;

Query Match 100.0%; Score 21; DB 5; Length 55;  
Best Local Similarity 100.0%; Pred. No. 4.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4  
DB 3 FGLM 6

RT environments.";  
RL Nucleic Acids Res. 30:3927-3935 (2002).  
DR EMBL; AF004602; BAC14682.1; --  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 58 AA; 6332 MW; 87EE8D5B5BA78AB CRC64;

Query Match 100.0%; Score 21; DB 16; Length 58;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4  
DB 21 FGLM 24

RESULT 8  
Q9GML1  
ID Q9GML1 PRELIMINARY; PRT; 63 AA.  
AC Q9GML1;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Hypothetical protein.  
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;  
OC Cercopitheidae; Macaca.  
OX NCBI\_TaxID=9541;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,  
RA Suzuki Y., Sugano S., Hashimoto K.;  
RT "Isolation of full-length cDNA clones from macaque brain cDNA  
RT libraries.";  
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB047938; BAB12349.1; --  
KW Hypothetical protein.  
SQ SEQUENCE 63 AA; 7040 MW; 9D31A5DF462ED22E CRC64;

Query Match 100.0%; Score 21; DB 6; Length 63;  
Best Local Similarity 100.0%; Pred. No. 4.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4  
DB 34 FGLM 37

RESULT 9  
Q82X04  
ID Q82X04 PRELIMINARY; PRT; 63 AA.  
AC Q82X04;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Hypothetical protein.  
GN NE0496.  
OS Nitrosomonas europaea.  
OC Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;  
OC Nitrosomonadaceae; Nitrosomonas.  
OX NCBI\_TaxID=915;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 19718 /IFO 14298;  
RX MEDLINE=22586410; PubMed=12700255;  
RA Chain P., Lamerdin J.E., Larimer F.W., Regala W., Lao V., Land M.,  
RA Hauser L., Hooper A.B., Klotz M.G., Norton J., Sayavedra-Soto L.A.,  
RA Arciero D.M., Hommes N.G., Whittaker M.M., Arp D.J.;  
RT "Complete genome sequence of the ammonia-oxidizing bacterium and  
RT obligate chemolithoautotroph Nitrosomonas europaea.";  
RL J. Bacteriol. 195:2759-2773 (2003).  
DR EMBL; BX321857; CAD84407.1; --

```

KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 63 AA; 7212 MW; D8098B79A1452DC5 CRC64;

Query Match 100.0%; Score 21; DB 16; Length 63;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4
Db 38 FGLM 41

RESULT 10
Q86H30 PRELIMINARY; PRT; 64 AA.
AC Q86H30;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelidida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
RX MEDLINE=22092622; PubMed=12097910;
RA Gloeckner G., Eichinger L., Szatranski K., Pachebat J., Dear P.,
RA Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K.,
RA Tungal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.;
RT "Sequence and analysis of chromosome 2 of Dictyostelium discoideum.";
RN Nature 418:79-85(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
RA Baumgart C.;
RA Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC115598; AAC53215.1; -.
KW Hypothetical protein.
SQ SEQUENCE 64 AA; 7451 MW; B0C0A0DB9DE71D7 CRC64;

Query Match 100.0%; Score 21; DB 5; Length 64;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4
Db 28 FGLM 31

RESULT 11
Q8GTG4 PRELIMINARY; PRT; 67 AA.
AC Q8GTG4;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE WRKY transcription factor IId-2 (Fragment).
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamnids; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Money Maker; TISSUE=Leaf;
RA Cagna G., Boes A., Ulker B., Zhou A., Wanke D., Somssich I.E.;
RT "Comparison of WRKY group II transcription factors from plants.";
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY157060; AAN71730.1; -.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR003657; WRKY.
DR Pfam; PF03106; WRKY; 1.

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DR PROSITE; PSS0811; WRKY; 1.
FT NON_TER 1
SQ SEQUENCE 67 AA; 7616 MW; D11A68FA7D715D92 CRC64;

Query Match 100.0%; Score 21; DB 10; Length 67;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4
Db 61 FGLM 64

RESULT 12
Q8TLX1 PRELIMINARY; PRT; 67 AA.
AC Q8TLX1;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Predicted protein.
GN MA2891.
OS Methanosarcina acetivorans.
OC Archaea; Euryarchaeota; Euryarchaeota orders incertae sedis;
OC Methanosarcinales; Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2214;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C2A / ATCC 35395 / DSM 2834;
RX MEDLINE=21929760; PubMed=11932338;
RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P., Brown A.,
RA Fitzhugh W., Calvo S., Engels R., Smirnov S., Atncor D., Johnson R.,
RA Allen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R.,
RA Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,
RA Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,
RA Hedderich R., Ingram-Smith C., Kuetner H.C., Krzycki J.A.,
RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
RA Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,
RA Perry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,
RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
RA Metcalf W.W., Birren B.;
RT "The genome of Methanosarcina acetivorans reveals extensive metabolic
RT and physiological diversity.";
RL Genome Res. 12:532-542(2002).
DR EMBL; AE010990; AAM06268.1; -.
KW Complete proteome.
SQ SEQUENCE 67 AA; 7934 MW; 644065037B1ECA32 CRC64;

Query Match 100.0%; Score 21; DB 17; Length 67;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4
Db 4 FGLM 7

RESULT 13
Q05625 PRELIMINARY; PRT; 68 AA.
AC Q05625;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE 5-enolpyruvylshikimate-3-phosphate synthase.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=8325-4;
RX MEDLINE=93381456; PubMed=8371108;
RA O'Connell C., Patten P.A., Foster T.J.;

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RT "Sequence and mapping of the araA gene of Staphylococcus aureus 8325-
RT 4."
RL J. Gen. Microbiol. 139:1449-1460 (1993).
RL ENBL; L05004; AAA71898.1; -
SQ SEQUENCE 68 AA; 7956 MW; 3B05C55134265B14 CRC64;

Query Match
Best Local Similarity 100.0%; Score 21; DB 2; Length 68;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4
Db 45 FGLM 48

RESULT 14
Q50886 PRELIMINARY; PRT; 68 AA.
AC Q50886;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Orf2 protein.
GN ORF2.
OS Myxococcus xanthus.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;
OC Cystobacterineae; Myxococcaceae; Myxococcus.
OX NCBI_TaxID=34;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=DK1050;
RX MEDLINE=96293442; PubMed=8692912;
RA Nicolas F.J., Cayuela M.L., Martinez-Argudo I.M., Ruiz-Vazquez R.M.,
RA Murillo F.J.;
RT "High mobility group I(Y)-like DNA-binding domains on a bacterial
RT transcription factor.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:6881-6885 (1996).
DR EMBL; Z56280; CAA91223.1; -
SQ SEQUENCE 68 AA; 7214 MW; 1FB0E21FB48BD763 CRC64;

Query Match
Best Local Similarity 100.0%; Score 21; DB 2; Length 68;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4
Db 10 FGLM 13

RESULT 15
Q9Y494 PRELIMINARY; PRT; 72 AA.
AC Q9Y494;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gamma preprotachykinin (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP SEQUENCE FROM N.A.
RC TISSUE=Blood, and Brain;
RA Lai J.P., Douglas S.D., Rappaport E., Wu J.M., Ho W.Z.;
RT "Identification of a Delta isoform of preprotachykinin mRNA in Human
RT Mononuclear Phagocytes and Lymphocytes.";
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF050657; AAC15703.1; -
DR GO; GO:0007268; P:synaptic transmission; IEA.
DR GO; GO:0007217; P:tachykinin signaling pathway; IEA.
DR InterPro; IPR008216; Protachykinin.
DR InterPro; IPR008215; Tachykinin.

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DR InterPro; IPR002040; Tachy Neurokinin.
DR Pfam; PF02202; Tachykinin_2.
DR ProDom; PD005598; Protachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 2.
FT NON_TER 1 1
FT NON_TER 72 72
SQ SEQUENCE 72 AA; 8274 MW; 2C02B2BA41EAAD16 CRC64;

Query Match
Best Local Similarity 100.0%; Score 21; DB 4; Length 72;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4
Db 30 FGLM 33

Search completed: August 25, 2004, 14:09:14
Job time : 126 secs

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Hand sheet



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 25, 2004, 13:40:49 ; Search time 123 seconds  
(without alignments)  
9.189 Million cell updates/sec

Title: US-10-053-669-2

Perfect score: 21

Sequence: 1 FGLM 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*

1: Geneseqp1980s:\*

2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	21	100.0	4	2	AAW41683	Aaw41683 Peptide u
2	21	100.0	4	2	AAy31075	Aay31075 Non-cross
3	21	100.0	4	3	AAb23026	Aab23026 Human/rat
4	21	100.0	4	3	AAy67577	Aay67577 P antagonist
5	21	100.0	4	4	AAb91447	Aab91447 Tachykini
6	21	100.0	4	5	ABb10091	Abb10091 Substance
7	21	100.0	4	5	AAU77846	Aau77846 Tachykini
8	21	100.0	5	2	AAr33009	Aar33009 Alpha-sub
9	21	100.0	5	2	AAr33008	Aar33008 Alpha-sub
10	21	100.0	5	2	AAr33007	Aar33007 Alpha-sub
11	21	100.0	5	2	AAr33010	Aar33010 Alpha-sub
12	21	100.0	5	2	AAr54549	Aar54549 Cholecyst
13	21	100.0	5	2	AAr54551	Aar54551 Cholecyst
14	21	100.0	5	2	AAr54550	Aar54550 Cholecyst
15	21	100.0	5	2	AAr54548	Aar54548 Cholecyst
16	21	100.0	5	2	AAW41687	Aaw41687 Tetrapept
17	21	100.0	5	2	AAW99643	Aaw99643 Substance
18	21	100.0	5	2	AAy50325	Aay50325 Neutrophil
19	21	100.0	5	2	AAW92660	Aaw92660 Human tac
20	21	100.0	5	2	AAW92702	Aaw92702 Human tac
21	21	100.0	5	3	AAb23025	Aab23025 Human/rat
22	21	100.0	5	3	AAy67576	Aay67576 P antagonist
23	21	100.0	5	4	AAb91428	Aab91428 Tachykini
24	21	100.0	5	4	AAb91389	Aab91389 Tachykini
25	21	100.0	5	5	ABb10090	Abb10090 Substance

## ALIGNMENTS

## RESULT 1

AAW41683

ID AAW41683 standard; peptide; 4 AA.

XX AAW41683;

DT 09-JUN-1998 (first entry)

XX Peptide used in ophthalmic drug to treat corneal disorders.

XX Ophthalmic drug; corneal disorder; ulcer; epithelial peeling; dry eye;

KW keratitis; insulin like growth factor-I; IGF-I; eye drop.

XX Synthetic.

OS Key

FH Key

FT Modified-site

FT Location/Qualifiers

XX 4

XX /note= "C-terminal amide"

XX WO9749419-Al.

XX 31-DEC-1997.

XX 11-JUN-1997; 97WO-JP002015.

XX 26-JUN-1996; 96JP-00165612.

XX (SANT ) SANTEN PHARM CO LTD.

XX Nishida T, Nakamura M, Nakata K;

XX WPI; 1998-076907/07.

XX Ophthalmic drug composition containing tetra:peptide - is useful as

XX corneal disorder remedy for corneal ulcer, corneal epithelial peeling,

XX dry eye, keratitis.

XX Claim 1; Page 15; 19pp; Japanese.

XX The present sequence represents a tetrapeptide which is the active

XX ingredient in an ophthalmic drug composition. It is used, together with

XX insulin like growth factor-I (IGF-I), to treat corneal disorders such as

XX corneal ulcer, corneal epithelial peeling, dry eye and keratitis. The

XX dosage is 0.1-5000 (preferably 1-1000) mg/day of the tetrapeptide and

XX 0.001-100 (preferably 0.01-10) mg/day of IGF-I. The preferable form of

XX the composition is eye drops

XX Sequence 4 AA;

SQ

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

Query Match 100.0%; Score 21; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGLM 4  
 ||||  
 Db 1 FGLM 4

RESULT 2  
 AAY31075  
 ID AAY31075 standard; peptide; 4 AA.

XX AC AAY31075;

XX DT 21-OCT-1999 (first entry)

XX DE Non-crosslinked protein particle peptide 124.

XX KW Non-crosslinked protein particle; diagnostic; therapy; monodisperse;  
 albumin; haemoglobin; nanometer; micrometer; clearance.

XX OS Synthetic.

XX FH Key Location/Qualifiers

XX FT Modified-site 4 /note= "C-terminal amide"

XX PN US5945033-A.

XX PD 31-AUG-1999.

XX PF 12-NOV-1996; 96US-00747137.

XX PR 15-JAN-1991; 91US-00641720.

XX PR 13-OCT-1992; 92US-00959560.

XX PR 01-JUN-1993; 93US-00069831.

XX PR 14-MAR-1994; 94US-00212546.

XX PA (HEMO-) HEMOSPHERE INC.

XX PI Yen RCK;

XX WP1; 1999-508153/42.

XX PT Non-crosslinked protein particles for therapeutic and diagnostic use.

XX PS Example 22; Col 103-104; 65pp; English.

XX CC This invention describes a novel aqueous suspension of monodisperse  
 CC particles on non-crosslinked, non-denatured albumin (50-5000 nm) which is  
 CC stable against dissolving upon dilution with an alcohol-free aqueous  
 CC medium. The method involves (a) forming an aqueous solution containing  
 CC albumin and hemoglobin and (b) treating the aqueous solution with an  
 CC alcohol to cause the solution to become turbid. The particles are useful  
 CC as agents for in vivo administration, either of their own administration  
 CC or as a vehicle for other therapeutic or diagnostic agents. The method  
 CC permits the formation of albumin and hemoglobin particles in the  
 CC nanometer and micrometer size range, in a form closer to their natural  
 CC form than the forms of the prior art. The particles therefore constitute  
 CC a more closely controlled agent for in vivo administration, with greater  
 CC ease of clearance from the body after their period of usefulness.  
 CC AAY30952-Y31135 represent peptides used in the method of the invention

XX SQ Sequence 4 AA;

Query Match 100.0%; Score 21; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGLM 4  
 ||||

Db 1 FGLM 4

RESULT 3

AAB23026

ID AAB23026 standard; peptide; 4 AA.

XX AC AAB23026;

XX DT 16-JAN-2001 (first entry)

XX DE Human/rat tachykinin Substance P C-terminal tetrapeptide.

XX KW Substance P; tachykinin; human; rat; magnesium binding defect;  
 sodium sensitive essential hypertension; insulin resistance;  
 type 2 diabetes; antibody; immunoassay; quantification.

XX OS Homo sapiens.

XX OS Rattus sp.

XX FH Key Location/Qualifiers

XX FT Modified-site 4 /note= "C-terminal amide"

XX PN W0200054053-A1.

XX PD 14-SEP-2000.

XX PF 09-MAR-2000; 2000WO-US003707.

XX PR 10-MAR-1999; 99US-00265690.

XX PA (WELL/) WELLS I C.

XX PI Wells IC;

XX WP1; 2000-587457/55.

XX PT Detecting magnesium binding defects associated with abnormal  
 physiological states such as sodium-sensitive essential hypertension and  
 type 2 insulin-resistant diabetes mellitus, comprises measuring a  
 specific pentapeptide in blood.

XX PS Disclosure; Page 5; 21pp; English.

XX CC The invention relates to a method for detecting magnesium binding  
 CC defects. The method comprises quantitating a tachykinin C-terminal  
 CC pentapeptide (e.g., AAB23025) and its degradation products (e.g.,  
 CC AAB23026) in blood using an antibody specific for the generalised  
 CC mammalian tachykinin C-terminal pentapeptide Phe-(Phe/Val)-Gly-Leu-Met-  
 CC NH2 (AAB23028). The method is useful for detecting cellular magnesium  
 CC binding defects which are associated with abnormal physiological states  
 CC such as sodium-sensitive essential hypertension and type 2 diabetes  
 CC mellitus. The present sequence represents the C-terminal 4 amino acids of  
 CC the tachykinin Substance P (AAB23027) from human and rat. This is a  
 CC degradation product of the Substance P C-terminal pentapeptide (AAB23025)  
 CC and may also be assayed according to the method of the invention

XX SQ Sequence 4 AA;

Query Match 100.0%; Score 21; DB 3; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGLM 4  
 ||||  
 Db 1 FGLM 4

RESULT 4

AAY67577

ID AAY67577 standard; peptide; 4 AA.

XX

AC AAY67577;  
 XX 19-MAY-2000 (first entry)  
 XX P antagonist peptide #5.  
 XX  
 XX Pharmaceutical; veterinary; gonadotropin-releasing hormone; GnRH;  
 KW pore-forming agent; lecithin; stearin; P antagonist.  
 XX Unidentified.  
 XX  
 XX Key Location/Qualifiers  
 FT Modified-site 4  
 FT /note= "C-terminal amide"  
 XX  
 PN WO200004897-A1.  
 XX  
 PD 03-FEB-2000.  
 XX  
 PF 20-JUL-1999; 99WO-AU000585.  
 XX  
 PR 20-JUL-1998; 98AU-00004730.  
 PR 20-JUL-1998; 98AU-00004731.  
 PR 13-MAY-1999; 99AU-00000324.  
 XX  
 PA (PEPT-) PEPTTECH LTD.  
 XX  
 PI Trigg TE, Walsh JD, Rathjen DA;  
 XX WPI; 2000-182528/16.  
 DR  
 XX Bioimplant formulation for sustained delivery of an active agent over 7  
 PT days to 2 years, comprises active agent, pore-forming agent and stearin.  
 PT  
 XX Claim 20; Page 21; 37pp; English.  
 PS  
 CC The invention provides a pharmaceutical and/or veterinary formulation  
 CC that comprises 2-30% of active agents which include a gonadotropin-  
 CC releasing hormone (GnRH) agonist, 0.5-20% of a pore-forming agent which  
 CC is not lecithin, and the remainder stearin. The formulation is useful as  
 CC a sustained release implant which can deliver the active agent for a  
 CC period of 7 days to 2 years. Sequences AAY67573-578 represent P  
 CC antagonist peptides used in the composition  
 XX  
 SQ Sequence 4 AA;  
 Query Match 100.0%; Score 21; DB 3; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FGLM 4  
 DB 1 FGLM 4  
 RESULT 5  
 AAB91447  
 ID AAB91447 standard; peptide; 4 AA.  
 AC AAB91447;  
 XX  
 XX 22-JUN-2001 (first entry)  
 DT Tachykinins peptide SEQ ID NO:623.  
 DE  
 XX Protection; endogenous therapeutic peptide; peptidase; conjugation;  
 KW blood component; modification; succinimidyl; maleimido group; amino;  
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.  
 XX  
 XX Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO2000069900-A2.

XX 23-NOV-2000.  
 XX 17-MAY-2000; 2000WO-US013576.  
 PF 17-MAY-1999; 99US-0134406P.  
 PR 10-SEP-1999; 99US-0153406P.  
 PR 15-OCT-1999; 99US-0159783P.  
 XX (CONJ-) CONJUCHEM INC.  
 PA  
 XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;  
 PI WPI; 2001-112059/12.  
 XX  
 DR Modifying and attaching therapeutic peptides to albumin prevents  
 PT peptidase degradation, useful for increasing length of in vivo activity.  
 PT  
 XX Disclosure; Page 402; 733pp; English.  
 PS  
 CC The present invention describes a modified therapeutic peptide (I)  
 CC comprising a therapeutically active amino acid region (III) and a  
 CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to  
 CC a less therapeutically active amino acid region (IV), which covalently  
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a  
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.  
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth  
 CC factors and neurotransmitters, to protect them from peptidase activity in  
 CC vivo for the treatment of various disorders. Endogenous therapeutic  
 CC peptides are not suitable as drug candidates as they require frequent  
 CC administration due to rapid degradation by peptidases in the body.  
 CC Modifying and attaching therapeutic peptides to albumin prevents or  
 CC reduces the action of peptidases to increase length of activity (half  
 CC life) and specificity as bonding to large molecules decreases  
 CC intracellular uptake and interference with physiological processes.  
 CC AAB90829 to AAB92441 represent peptides which can be used in the  
 CC exemplification of the present invention  
 XX  
 SQ Sequence 4 AA;  
 Query Match 100.0%; Score 21; DB 4; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FGLM 4  
 DB 1 FGLM 4  
 RESULT 6  
 ABB10091  
 ID ABB10091 standard; peptide; 4 AA.  
 XX  
 AC ABB10091;  
 XX  
 XX 26-JUL-2002 (first entry)  
 DT Substance P analog used in wound healing treatment#14.  
 XX  
 DE Wound healing; insulin-like growth factor-I; tear; abrasion; skin ulcer;  
 KW surgical incision; burn.  
 XX  
 XX Unidentified.  
 OS  
 XX WO200213853-A1.  
 PN  
 PD 21-FEB-2002.  
 XX  
 XX 10-AUG-2001; 2001WO-JP006933.  
 PF  
 XX 10-AUG-2000; 2000JP-00242489.  
 PR  
 XX 28-NOV-2000; 2000JP-003611388.  
 XX

PA (SANT ) SANTEN PHARM CO LTD.  
PA (NISH/) NISHIDA T.  
XX Nishida T, Nakata K, Nakamura M;  
XX WPI; 2002-269153/31.  
DR  
XX Skin wound healing promoters or skin epidermal extension promoters  
PT containing substance P analogs and insulin-like growth factor-I for  
PT treating wounds like tear, abrasion, surgical incision, skin ulcers or  
PT burns.  
XX  
XX Claim 3; Page 11; 20pp; Japanese.  
PS  
XX The invention relates to skin wound healing promoters, containing  
CC substance P analogs or their pharmaceutically-acceptable salts, and  
CC insulin-like growth factor-I as the active ingredient. The promoters are  
CC for treating wounds like tears, abrasions, surgical incisions, or skin  
CC ulcers and burns. The current sequence represents a substance P analog  
CC for use in wound healing treatment  
XX  
XX Sequence 4 AA;  
SQ  
Query Match 100.0%; Score 21; DB 5; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FGLM 4  
Db 1 FGLM 4  
RESULT 7  
AAU77846  
ID AAU77846 standard; peptide; 4 AA.  
XX  
XX AAU77846;  
AC  
XX  
XX 05-JUN-2002 (first entry)  
DT  
XX Tachykinin N -terminal tetrapeptide.  
DE  
XX Tachykinin; substance P; hypertension; hypotensive; antidiabetic;  
XX gynaecological; salt-insensitive hypertension; magnesium binding;  
KW insulin resistance; type 2 diabetes mellitus; pre-eclampsia; eclampsia.  
XX  
XX Homo sapiens.  
OS  
XX  
XX Key Location/Qualifiers  
FH Modified-site 4.4  
FT /note= "C terminal-amide"  
FT  
XX  
XX WO200211714-A2.  
PN  
XX  
XX 14-FEB-2002.  
PD  
XX  
XX 09-AUG-2001; 2001WO-US024909.  
PF  
XX  
XX 09-AUG-2000; 2000US-00635266.  
PR  
XX  
XX (MAGN-) MAGNESIUM DIAGNOSTICS INC.  
PA  
XX  
XX Wells IC;  
PI  
XX  
XX WPI; 2002-280663/32.  
DR  
XX  
XX New mono-peptides derived from butadienes, ethylenes and propanes are  
PT magnesium binding defect antagonists, useful in the treatment of e.g.  
PT hypertension, insulin resistance of type 2 diabetes mellitus and  
PT eclampsia.  
PT  
XX  
XX Disclousure; Page 2; 38pp; English.  
PS  
XX

CC This invention relates to novel therapeutic compounds and methods used  
CC for treating mammals with disorders such as salt-insensitive  
CC hypertension. The mono-peptide compounds of the invention are derived from  
CC butadienes, ethylenes and propanes. The compounds of the invention are  
CC used to correct a defect in magnesium binding within the plasma membranes  
CC of somatic cells which results in a decrease in the intracellular  
CC concentration of magnesium ions. These compounds may be used in the  
CC treatment of a mammal affected with magnesium binding defect, salt-  
CC sensitive (particularly hypertension), insulin resistance of type 2  
CC diabetes mellitus and pre-eclampsia/eclampsia. The compounds of the  
CC invention have an advantage over prior art compounds in that these  
CC compounds are biologically stable. The present sequence represents the a  
CC tetrapeptide from the C terminal sequence of tachykinin known as  
CC substance P, this peptide is sufficient to correct the magnesium binding  
CC defect responsible for causing hypertension  
XX  
XX Sequence 4 AA;  
SQ  
Query Match 100.0%; Score 21; DB 5; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FGLM 4  
Db 1 FGLM 4  
RESULT 8  
AAR33009  
ID AAR33009 standard; peptide; 5 AA.  
XX  
XX AAR33009;  
AC  
XX  
XX 25-MAR-2003 (revised)  
DT  
XX 02-APR-1993 (first entry)  
DT  
XX Alpha-substituted short peptide.  
DE  
XX  
XX CCK; neuropeptide; endorphin; hormone; LHRH; contraception; analgesia;  
KW improved bioavailability.  
KW  
XX  
XX Synthetic.  
OS  
XX  
XX Key Location/Qualifiers  
FH Modified-site 4  
FT /note= "alpha-Me-Leu"  
FT Modified-site 5  
FT /note= "Met-NH2"  
FT  
XX  
XX WO9219254-A1.  
PN  
XX  
XX 12-NOV-1992.  
PD  
XX  
XX 15-APR-1992; 92WO-US003119.  
PF  
XX  
XX 24-APR-1991; 91US-00690755.  
PR  
XX 20-MAR-1992; 92US-00852086.  
PR  
XX  
XX (WARN ) WARNER LAMBERT CO.  
PA  
XX  
XX Horwell DC, Hughes J, Richardson RS, Howson W;  
XX WPI; 1992-398522/48.  
DR  
XX  
XX New alpha-substd. polypeptide are e.g. selective receptor ligands - for  
PT treating inflammation, pain, stroke, ulcers, hypertension, heart failure,  
PT depression, cancer, asthma, psychosis, arthritis, etc.  
PT  
XX  
XX Claim 3; Page 41; 46pp; English.  
PS  
XX  
XX The peptide is a specifically claimed example of a group of generically  
CC claimed mono-, di-, tri-, tetra- and penta-peptides which include a  
CC substituent on an alpha-C atom in the chain. Such substitution may modify

CC the bioavailability, stability or absorbability of the peptide and hence  
 CC may improve the activity of the peptide as a drug. Depending on the  
 CC nature of the parent peptide (hormone, endorphin, CCK, NK2, chemotactic  
 CC peptide, etc.), the modified peptides are variously useful for treating  
 CC obesity, anxiety, gastrointestinal ulcers, pain, stroke, inflammation,  
 CC addictive drug withdrawal symptoms, hypertension, heart failure,  
 CC cognition or memory disorders, spasticity, depression, diabetes, cancer,  
 CC asthma, bladder dysfunction, psychosis and arthritis; and as  
 CC contraceptives. (Updated on 25-MAR-2003 to correct PN field.) (Updated on  
 CC 25-MAR-2003 to correct PD field.) (Updated on 25-MAR-2003 to correct PR  
 CC field.) (Updated on 25-MAR-2003 to correct PI field.)

SQ Sequence 5 AA;

Query Match 100.0%; Score 21; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4  
 Db 1 1111  
 2 FGLM 5

# RESULT 9

AAR33008  
 ID AAR33008 standard; peptide; 5 AA.

XX AAR33008;  
 AC AAR33008;

XX 25-MAR-2003 (revised)  
 DT 02-APR-1993 (first entry)

DE Alpha-substituted short peptide.

XX CCK; neuropeptide; endorphin; hormone; LHRH; contraception; analgesia;  
 KW improved bioavailability.  
 OS Synthetic.

XX Key Location/Qualifiers  
 FH Modified-site 2 /note= "alpha-Me-Phe"  
 FT Modified-site 5 /note= "Met-NH2"  
 FT Modified-site 5 /note= "Met-NH2"

XX WO9219254-A1.

XX 12-NOV-1992.

XX 15-APR-1992; 92WO-US003119.

XX 24-APR-1991; 91US-00690755.  
 PR 20-MAR-1992; 92US-00852086.

XX (WARN ) WARNER LAMBERT CO.  
 PA Horwell DC, Hughes J, Richardson RS, Howson W;

XX WPI; 1992-398522/48.

XX New alpha-subst. polypeptide are e.g. selective receptor ligands - for  
 PT treating inflammation, pain, stroke, ulcers, hypertension, heart failure,  
 PT depression, cancer, asthma, psychosis, arthritis, etc.

XX Claim 3; Page 41; 46pp; English.

XX The peptide is a specifically claimed example of a group of generically  
 CC claimed mono-, di-, tri-, tetra- and penta-peptides which include a  
 CC substituent on an alpha-C atom in the chain. Such substitution may modify  
 CC the bioavailability, stability or absorbability of the peptide and hence  
 CC may improve the activity of the peptide as a drug. Depending on the  
 CC nature of the parent peptide (hormone, endorphin, CCK, NK2, chemotactic  
 CC peptide, etc.), the modified peptides are variously useful for treating

CC obesity, anxiety, gastrointestinal ulcers, pain, stroke, inflammation,  
 CC addictive drug withdrawal symptoms, hypertension, heart failure,  
 CC cognition or memory disorders, spasticity, depression, diabetes, cancer,  
 CC asthma, bladder dysfunction, psychosis and arthritis; and as  
 CC contraceptives. (Updated on 25-MAR-2003 to correct PN field.) (Updated on  
 CC 25-MAR-2003 to correct PD field.) (Updated on 25-MAR-2003 to correct PR  
 CC field.) (Updated on 25-MAR-2003 to correct PI field.)

SQ Sequence 5 AA;

Query Match 100.0%; Score 21; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4  
 Db 1 1111  
 2 FGLM 5

# RESULT 10

AAR33007  
 ID AAR33007 standard; peptide; 5 AA.

XX AAR33007;  
 AC AAR33007;

XX 25-MAR-2003 (revised)  
 DT 02-APR-1993 (first entry)

DE Alpha-substituted short peptide.

XX CCK; neuropeptide; endorphin; hormone; LHRH; contraception; analgesia;  
 KW improved bioavailability.  
 OS Synthetic.

XX Key Location/Qualifiers  
 FH Modified-site 1 /note= "alpha-Me-Phe"  
 FT Modified-site 5 /note= "Met-NH2"  
 FT Modified-site 5 /note= "Met-NH2"

XX WO9219254-A1.

XX 12-NOV-1992.

XX 15-APR-1992; 92WO-US003119.

XX 24-APR-1991; 91US-00690755.  
 PR 20-MAR-1992; 92US-00852086.

XX (WARN ) WARNER LAMBERT CO.  
 PA Horwell DC, Hughes J, Richardson RS, Howson W;

XX WPI; 1992-398522/48.

XX New alpha-subst. polypeptide are e.g. selective receptor ligands - for  
 PT treating inflammation, pain, stroke, ulcers, hypertension, heart failure,  
 PT depression, cancer, asthma, psychosis, arthritis, etc.

XX Claim 3; Page 41; 46pp; English.

XX The peptide is a specifically claimed example of a group of generically  
 CC claimed mono-, di-, tri-, tetra- and penta-peptides which include a  
 CC substituent on an alpha-C atom in the chain. Such substitution may modify  
 CC the bioavailability, stability or absorbability of the peptide and hence  
 CC may improve the activity of the peptide as a drug. Depending on the  
 CC nature of the parent peptide (hormone, endorphin, CCK, NK2, chemotactic  
 CC peptide, etc.), the modified peptides are variously useful for treating  
 CC obesity, anxiety, gastrointestinal ulcers, pain, stroke, inflammation,  
 CC addictive drug withdrawal symptoms, hypertension, heart failure,  
 CC cognition or memory disorders, spasticity, depression, diabetes, cancer,  
 CC asthma, bladder dysfunction, psychosis and arthritis; and as

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CC contraceptives. (Updated on 25-MAR-2003 to correct PN field.) (Updated on  
CC 25-MAR-2003 to correct PD field.) (Updated on 25-MAR-2003 to correct PR  
CC field.) (Updated on 25-MAR-2003 to correct PI field.)

XX Sequence 5 AA;

Query Match 100.0%; Score 21; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4  
Db 2 FGLM 5

RESULT 11  
AAR33010  
ID AAR33010 standard; peptide; 5 AA.

XX AAR33010;  
AC  
XX 25-MAR-2003 (revised)  
DT 02-APR-1993 (first entry)  
XX

DE Alpha-substituted short peptide.

XX CCK; neuropeptide; endorphin; hormone; LHRH; contraception; analgesia;  
KW improved bioavailability.

XX Synthetic.

XX Key Location/Qualifiers  
FH Modified-site 5 /note= "alpha-Me-Met-NH2"  
FT  
FT  
XX

XX WO9219254-A1.

XX 12-NOV-1992.

XX 15-APR-1992; 92WO-US003119.

XX 24-APR-1991; 91US-00690755.

XX 20-MAR-1992; 92US-00852086.

XX (WARN ) WARNER LAMBERT CO.

XX Horwell DC, Hughes J, Richardson RS, Howson W;

XX WPI; 1992-398522/48.

XX New alpha-substd. polypeptide are e.g. selective receptor ligands - for  
XX treating inflammation, pain, stroke, ulcers, hypertension, heart failure,  
XX depression, cancer, asthma, psychosis, arthritis, etc.

XX Claim 3; Page 41; 46pp; English.

XX The peptide is a specifically claimed example of a group of generically  
XX claimed mono-, di-, tri-, tetra- and penta-peptides which include a  
XX substituent on an alpha-C atom in the chain. Such substitution may modify  
XX the bioavailability, stability or absorbability of the peptide and hence  
XX may improve the activity of the peptide as a drug. Depending on the  
XX nature of the parent peptide (hormone, endorphin, CCK, NK2, chemotactic  
XX peptide, etc.), the modified peptides are variously useful for treating,  
XX obesity, anxiety, gastrointestinal ulcers, pain, stroke, inflammation,  
XX addictive drug withdrawal symptoms, hypertension, heart failure,  
XX cognition or memory disorders, spasticity, depression, diabetes, cancer,  
XX asthma, bladder dysfunction, psychosis and arthritis; and as  
XX contraceptives. (Updated on 25-MAR-2003 to correct PN field.) (Updated on  
XX 25-MAR-2003 to correct PD field.) (Updated on 25-MAR-2003 to correct PR  
XX field.) (Updated on 25-MAR-2003 to correct PI field.)

XX Sequence 5 AA;

Query Match 100.0%; Score 21; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4  
Db 2 FGLM 5

RESULT 12  
AAR54549  
ID AAR54549 standard; peptide; 5 AA.

XX AAR54549;

XX 25-MAR-2003 (revised)

DT 14-DEC-1994 (first entry)

XX Cholecystokinin analogue peptide #42.

XX Peptide analogue; peptoid; cholecystokinin; CCK; obesity; anxiety;  
KW gastrointestinal ulcers; pain; stroke; inflammation; hypertension;  
KW heart failure; cognition; memory enhancement; spasticity; depression;  
KW diabetes; cancers; asthma; bladder dysfunction; psychosis; arthritis.

XX Synthetic.

XX Key Location/Qualifiers  
FH Modified-site 2 /label= MePhe  
FT Modified-site 5 /note= "Amidated C-terminal"  
FT  
FT  
XX

XX WO9409031-A1.

XX 28-APR-1994.

XX 14-OCT-1993; 93WO-US009809.

XX 19-OCT-1992; 92US-00963169.

XX 08-OCT-1993; 93US-00131693.

XX (WARN ) WARNER LAMBERT CO.

XX Horwell DC, Howson W, Hughes J, Richardson RS;

XX WPI; 1994-151243/18.

XX New cholecystokinin analogues - useful e.g. in treatment of pain,  
XX obesity, stroke, anxiety, and gastrointestinal ulcers.

XX Claim 3; Page 66; 73pp; English.

XX The sequences given in AAR53117-38 and AAR54530-51 are peptide analogues  
XX of cholecystokinin (CCK) which can be used to treat obesity, anxiety,  
XX gastrointestinal ulcers, pain, stroke, inflammation, hypertension, heart  
XX failure, cognition, memory enhancement, spasticity, depression, diabetes,  
XX cancers, asthma, bladder dysfunction, psychosis, arthritis and in the  
XX treatment of substance withdrawal. (Updated on 25-MAR-2003 to correct PN  
XX field.)

XX Sequence 5 AA;

Query Match 100.0%; Score 21; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4  
Db 2 FGLM 5

RESULT 13

```

AAR54551
ID AAR54551 standard; peptide; 5 AA.
XX
AC AAR54551;
XX
DT 25-MAR-2003 (revised)
DT 14-DEC-1994 (first entry)
XX
DE Cholecystokinin analogue peptide #44.
XX
KW Peptide analogue; peptoid; cholecystokinin; CCK; obesity; anxiety;
KW gastrointestinal ulcers; pain; stroke; inflammation; hypertension;
KW heart failure; cognition; memory enhancement; spasticity; depression;
KW diabetes; cancers; asthma; bladder dysfunction; psychosis; arthritis.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 5
FT FT /label= MeMet
FT FT /note= "Amidated C-terminal"
XX
PN WO9409031-A1.
XX
PD 28-APR-1994.
XX
PF 14-OCT-1993; 93WO-US009809.
XX
PR 19-OCT-1992; 92US-00963169.
PR 08-OCT-1993; 93US-00131693.
XX
XX (WARN ) WARNER LAMBERT CO.
XX
PI Horwell DC, Howson W, Hugues J, Richardson RS;
XX
DR WPI; 1994-151243/18.
XX
PT New cholecystokinin analogues - useful e.g. in treatment of pain,
PT obesity, stroke, anxiety, and gastrointestinal ulcers.
XX
PS Claim 3; Page 66; 73pp; English.
XX
CC The sequences given in AAR53117-38 and AAR54530-51 are peptide analogues
CC of cholecystokinin (CCK) which can be used to treat obesity, anxiety,
CC gastrointestinal ulcers, pain, stroke, inflammation, hypertension, heart
CC failure, cognition, memory enhancement, spasticity, depression, diabetes,
CC cancers, asthma, bladder dysfunction, psychosis, arthritis and in the
CC treatment of substance withdrawal. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
SQ Sequence 5 AA;
Query Match 100.0%; Score 21; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. NO. 1.4e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4
Db |||||
2 FGLM 5

RESULT 14
AAR54550
ID AAR54550 standard; peptide; 5 AA.
XX
AC AAR54550;
XX
DT 25-MAR-2003 (revised)
DT 14-DEC-1994 (first entry)
XX
DE Cholecystokinin analogue peptide #43.
XX
KW Peptide analogue; peptoid; cholecystokinin; CCK; obesity; anxiety;
XX
KW gastrointestinal ulcers; pain; stroke; inflammation; hypertension;
XX heart failure; cognition; memory enhancement; spasticity; depression;
XX diabetes; cancers; asthma; bladder dysfunction; psychosis; arthritis.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT FT /label= MePhe
FT FT Modified-site 5

AAR54551
ID AAR54551 standard; peptide; 5 AA.
XX
AC AAR54551;
XX
DT 25-MAR-2003 (revised)
DT 14-DEC-1994 (first entry)
XX
DE Cholecystokinin analogue peptide #44.
XX
KW Peptide analogue; peptoid; cholecystokinin; CCK; obesity; anxiety;
KW gastrointestinal ulcers; pain; stroke; inflammation; hypertension;
KW heart failure; cognition; memory enhancement; spasticity; depression;
KW diabetes; cancers; asthma; bladder dysfunction; psychosis; arthritis.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 3
FT FT /label= MeLeu
FT FT Modified-site 5
FT FT /note= "Amidated C-terminal"
XX
PN WO9409031-A1.
XX
PD 28-APR-1994.
XX
PF 14-OCT-1993; 93WO-US009809.
XX
PR 19-OCT-1992; 92US-00963169.
PR 08-OCT-1993; 93US-00131693.
XX
XX (WARN ) WARNER LAMBERT CO.
XX
PI Horwell DC, Howson W, Hugues J, Richardson RS;
XX
DR WPI; 1994-151243/18.
XX
PT New cholecystokinin analogues - useful e.g. in treatment of pain,
PT obesity, stroke, anxiety, and gastrointestinal ulcers.
XX
PS Claim 3; Page 66; 73pp; English.
XX
CC The sequences given in AAR53117-38 and AAR54530-51 are peptide analogues
CC of cholecystokinin (CCK) which can be used to treat obesity, anxiety,
CC gastrointestinal ulcers, pain, stroke, inflammation, hypertension, heart
CC failure, cognition, memory enhancement, spasticity, depression, diabetes,
CC cancers, asthma, bladder dysfunction, psychosis, arthritis and in the
CC treatment of substance withdrawal. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
SQ Sequence 5 AA;
Query Match 100.0%; Score 21; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. NO. 1.4e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4
Db |||||
2 FGLM 5

RESULT 15
AAR54548
ID AAR54548 standard; peptide; 5 AA.
XX
AC AAR54548;
XX
DT 25-MAR-2003 (revised)
DT 14-DEC-1994 (first entry)
XX
DE Cholecystokinin analogue peptide #41.
XX
KW Peptide analogue; peptoid; cholecystokinin; CCK; obesity; anxiety;
KW gastrointestinal ulcers; pain; stroke; inflammation; hypertension;
KW heart failure; cognition; memory enhancement; spasticity; depression;
KW diabetes; cancers; asthma; bladder dysfunction; psychosis; arthritis.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT FT /label= MePhe
FT FT Modified-site 5

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FT /note= "Amidated C-terminal"

XX PN WO9409031-A1.  
XX PD 28-APR-1994.  
XX PF 14-OCT-1993; 93WO-US009809.  
XX PR 19-OCT-1992; 92US-00963169.  
XX PR 08-OCT-1993; 93US-00131693.  
XX PA (WARN ) WARNER LAMBERT CO.  
XX PI Horwell DC, Howson W, Hugues J, Richardson RS;  
XX DR WPI; 1994-151243/18.  
XX PT New cholecystokinin analogues - useful e.g. in treatment of pain,  
XX PT obesity, stroke, anxiety, and gastrointestinal ulcers.  
XX PS Claim 3; Page 66; 73pp; English.  
XX CC The sequences given in AAR53117-38 and AAR54530-51 are peptide analogues  
XX CC of cholecystokinin (CCK) which can be used to treat obesity, anxiety,  
XX CC gastrointestinal ulcers, pain, stroke, inflammation, hypertension, heart  
XX CC failure, cognition, memory enhancement, spasticity, depression, diabetes,  
XX CC cancers, asthma, bladder dysfunction, psychosis, arthritis and in the  
XX CC treatment of substance withdrawal. (Updated on 25-MAR-2003 to correct PN  
XX CC field.)  
XX SQ Sequence 5 AA;

Query Match 100.0%; Score 21; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4  
Db 2 FGLM 5

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Job time : 126 secs



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OM protein - protein search, using sw model

Run on: August 25, 2004, 14:07:19 ; Search time 127 Seconds  
(without alignments)  
9.909 Million cell updates/sec

Title: US-10-053-669-2  
Perfect score: 21  
Sequence: 1 FGLM 4

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1297172 seqs, 314612898 residues

Total number of hits satisfying chosen parameters: 1297172

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	4	14	US-10-230-133-3
2	21	100.0	4	14	US-10-053-669-2
3	21	100.0	4	16	US-10-695-536-3
4	21	100.0	5	12	US-10-134-187-3
5	21	100.0	5	14	US-10-053-669-1
6	21	100.0	5	16	US-10-688-741-3
7	21	100.0	5	16	US-10-346-737A-30
8	21	100.0	6	14	US-10-168-789A-38
9	21	100.0	7	12	US-10-134-187-2
10	21	100.0	7	14	US-10-036-542-110
11	21	100.0	7	14	US-10-036-542-111
12	21	100.0	7	14	US-10-168-789A-37
13	21	100.0	7	16	US-10-688-741-2
14	21	100.0	8	14	US-10-168-789A-36
15	21	100.0	9	12	US-10-134-187-1

16	21	100.0	9	14	US-10-036-542-112
17	21	100.0	9	14	US-10-168-789A-35
18	21	100.0	9	16	US-10-390-472-6
19	21	100.0	9	16	US-10-688-741-1
20	21	100.0	10	14	US-10-168-789A-34
21	21	100.0	11	9	US-09-935-682-64
22	21	100.0	11	10	US-09-988-792-1
23	21	100.0	11	10	US-09-988-792-6
24	21	100.0	11	10	US-09-988-792-7
25	21	100.0	11	10	US-09-988-792-8
26	21	100.0	11	10	US-09-988-792-10
27	21	100.0	11	12	US-09-841-091B-26
28	21	100.0	11	12	US-10-343-654-27
29	21	100.0	11	13	US-10-002-593-4
30	21	100.0	11	14	US-10-230-133-1
31	21	100.0	11	14	US-10-053-669-3
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34	21	100.0	11	14	US-10-197-954-130
35	21	100.0	11	14	US-10-251-703-25
36	21	100.0	11	14	US-10-168-789A-17
37	21	100.0	11	14	US-10-423-714-4
38	21	100.0	11	15	US-10-289-009-24
39	21	100.0	11	15	US-10-289-009-25
40	21	100.0	11	15	US-10-289-009-26
41	21	100.0	11	16	US-10-167-627-65
42	21	100.0	11	16	US-10-695-536-1
43	21	100.0	12	9	US-09-922-093-2
44	21	100.0	12	9	US-09-922-093-5
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ALIGNMENTS

RESULT 1  
US-10-230-133-3  
; Sequence 3, Application US/10230133  
; Publication No. US20030040625A1  
; GENERAL INFORMATION:  
; APPLICANT: Wells, Ibert  
; TITLE OF INVENTION: Antagonists of the magnesium binding defect as therapy agents and methods for treatment of abnormal physiological states  
; FILE REFERENCE: 2892-106  
; CURRENT APPLICATION NUMBER: US/10/230,133  
; PRIOR FILING DATE: 2002-08-29  
; PRIOR APPLICATION NUMBER: 09/635,266  
; PRIOR FILING DATE: 2000-08-09  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 3  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MOD.RES  
; LOCATION: (4)..(4)  
; OTHER INFORMATION: AMIDATION  
US-10-230-133-3

Query Match 100.0%; Score 21; DB 14; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGLM 4  
Db 1 FGLM 4

RESULT 2  
US-10-053-669-2  
; Sequence 2, Application US/10053669  
; Publication No. US20030077658A1

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; GENERAL INFORMATION:
; APPLICANT: Wells, Ibert
; TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound Ma
; TITLE OF INVENTION: for Disease Diagnosis
; FILE REFERENCE: N1427-005
; CURRENT APPLICATION NUMBER: US/10/053,669
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 09/265,690
; PRIOR FILING DATE: 1999-03-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (4)-(4)
; OTHER INFORMATION: AMIDATION
US-10-053-669-2

Query Match          100.0%; Score 21; DB 14; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGLM 4
Db 1 FGLM 4

RESULT 3
US-10-695-536-3
; Sequence 3, Application US/10695536
; Publication No. US20040110692A1
; GENERAL INFORMATION:
; APPLICANT: Wells, Ibert Clifton
; TITLE OF INVENTION: Antagonists of the Magnesium Binding Defect as Therapeutic Agents
; TITLE OF INVENTION: and Methods for Treatment of Abnormal Physiological States
; FILE REFERENCE: 800812-0008
; CURRENT APPLICATION NUMBER: US/10/695,536
; CURRENT FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: US 10/230,133
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 09/635,266
; PRIOR FILING DATE: 2000-08-09
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (4)-(4)
; OTHER INFORMATION: AMIDATION
US-10-695-536-3

Query Match          100.0%; Score 21; DB 16; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGLM 4
Db 1 FGLM 4

RESULT 4
US-10-134-187-3
; Sequence 3, Application US/10134187
; Publication No. US20030202981A1
; GENERAL INFORMATION:
; APPLICANT: Kream, Richard M.
; APPLICANT: Kream, Richard M.
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; APPLICANT: Kream, Richard M.
; TITLE OF INVENTION: Chimeric Hybrid Analgesics
; FILE REFERENCE: Kream
; CURRENT APPLICATION NUMBER: US/10/134,187
; CURRENT FILING DATE: 2002-04-26
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 5
; TYPE: PRT
; ORGANISM: mammalian
US-10-134-187-3

Query Match          100.0%; Score 21; DB 12; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGLM 4
Db 2 FGLM 5

RESULT 5
US-10-053-669-1
; Sequence 1, Application US/10053669
; Publication No. US2003007658A1
; GENERAL INFORMATION:
; APPLICANT: Wells, Ibert
; TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound Ma
; TITLE OF INVENTION: for Disease Diagnosis
; FILE REFERENCE: N1427-005
; CURRENT APPLICATION NUMBER: US/10/053,669
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 09/265,690
; PRIOR FILING DATE: 1999-03-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (5)-(5)
; OTHER INFORMATION: AMIDATION
US-10-053-669-1

Query Match          100.0%; Score 21; DB 14; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGLM 4
Db 2 FGLM 5

RESULT 6
US-10-688-741-3
; Sequence 3, Application US/10688741
; Publication No. US20040106636A1
; GENERAL INFORMATION:
; APPLICANT: Kream, Richard M.
; APPLICANT: Kream, Richard M.
; APPLICANT: Kream, Richard M.
; TITLE OF INVENTION: Method Of Inhibiting Opioid Tolerance Development With Chimeric
; FILE REFERENCE: Kream
; CURRENT APPLICATION NUMBER: US/10/688,741
; CURRENT FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 5
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; TYPE: PRT
; ORGANISM: mammalian
US-10-688-741-3

Query Match      100.0%; Score 21; DB 16; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4
Db 2 FGLM 5

RESULT 7
US-10-346-737A-30
; Sequence 30, Application US/10346737A
; Publication No. US20040142379A1
; GENERAL INFORMATION:
; APPLICANT: St. Hilaire, Phaedria
; TITLE OF INVENTION: AFFINITY FISHING FOR LIGANDS AND PROTEIN RECEPTORS
; FILE REFERENCE: 11225.16US01
; CURRENT APPLICATION NUMBER: US/10/346,737A
; CURRENT FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 30
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide
; NAME/KEY: MISC FEATURE
; LOCATION: (1)-(1)
; OTHER INFORMATION: Xaa is T(Sa)
US-10-346-737A-30

Query Match      100.0%; Score 21; DB 16; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4
Db 2 FGLM 5

US-10-168-789A-38
; Sequence 38, Application US/10168789A
; Publication No. US20030148943A1
; GENERAL INFORMATION:
; APPLICANT: ITOH, Yasuaki
; APPLICANT: NISHI, Kazunori
; APPLICANT: KITADA, Chieko
; APPLICANT: INATOMI, No. US20030148943A1uhiro
; TITLE OF INVENTION: No. US20030148943A1el Tachykinin-like Polypeptides and Use Thereof
; FILE REFERENCE: 2680USOP
; CURRENT APPLICATION NUMBER: US/10/168,789A
; CURRENT FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: PCT/JPO00/09083
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: JP 11-362638
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: JP 12-066714
; PRIOR FILING DATE: 1999-03-10
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 38
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide
US-10-168-789A-38

Query Match      100.0%; Score 21; DB 14; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4
Db 3 FGLM 6

RESULT 9
US-10-134-187-2
; Sequence 2, Application US/10134187
; Publication No. US20030202981A1
; GENERAL INFORMATION:
; APPLICANT: Kream, Richard M.
; APPLICANT: Kream, Richard M.
; APPLICANT: Kream, Richard M.
; TITLE OF INVENTION: Chimeric Hybrid Analgesics
; FILE REFERENCE: Kream
; CURRENT APPLICATION NUMBER: US/10/134,187
; CURRENT FILING DATE: 2002-04-26
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2
; LENGTH: 7
; TYPE: PRT
; ORGANISM: mammalian
US-10-134-187-2

Query Match      100.0%; Score 21; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4
Db 4 FGLM 7

RESULT 10
US-10-036-542-110
; Sequence 110, Application US/10036542
; Publication No. US20030083481A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: 25 Human Prostate and Prostate Cancer Associated Proteins
; FILE REFERENCE: PA002P1
; CURRENT APPLICATION NUMBER: US/10/036,542
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: PCT/US00/19666
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: 60/144,972
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: 60/148,681
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: 60/149,173
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/158,004
; PRIOR FILING DATE: 1999-10-06
; PRIOR APPLICATION NUMBER: 60/194,689
; PRIOR FILING DATE: 2000-04-05
; NUMBER OF SEQ ID NOS: 157
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 110
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-036-542-110

Query Match      100.0%; Score 21; DB 14; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 FGLM 4
Db      4 FGLM 7

Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 11
US-10-036-542-111
; Sequence 111, Application US/10036542
; Publication No. US20030083481A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: 25 Human Prostate and Prostate Cancer Associated Proteins
; FILE REFERENCE: PA002P1
; CURRENT APPLICATION NUMBER: US/10/036,542
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: PCT/US00/19666
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: 60/144,972
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: 60/148,681
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: 60/149,173
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/158,004
; PRIOR FILING DATE: 1999-10-06
; PRIOR APPLICATION NUMBER: 60/194,689
; PRIOR FILING DATE: 2000-04-05
; NUMBER OF SEQ ID NOS: 157
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 111
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-036-542-111

Query Match      100.0%; Score 21; DB 14; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FGLM 4
Db      2 FGLM 5

RESULT 12
US-10-168-789A-37
; Sequence 37, Application US/10168789A
; Publication No. US20030148943A1
; GENERAL INFORMATION:
; APPLICANT: ITOH, Yasuaki
; APPLICANT: NISHI, Kazunori
; APPLICANT: KITADA, Chieko
; APPLICANT: INATOMI, No. US20030148943A1uhiro
; TITLE OF INVENTION: No. US20030148943A1el Tachykinin-like Polypeptides and Use Thereo
; FILE REFERENCE: 2680USOP
; CURRENT APPLICATION NUMBER: US/10/168,789A
; CURRENT FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: PCT/JP00/09083
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: JP 11-362638
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: JP 12-066714
; PRIOR FILING DATE: 1999-03-10
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 37
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide
US-10-168-789A-37

Query Match      100.0%; Score 21; DB 14; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FGLM 4
Db      5 FGLM 8

US-10-168-789A-36
; Sequence 36, Application US/10168789A
; Publication No. US20030148943A1
; GENERAL INFORMATION:
; APPLICANT: ITOH, Yasuaki
; APPLICANT: NISHI, Kazunori
; APPLICANT: KITADA, Chieko
; APPLICANT: INATOMI, No. US20030148943A1uhiro
; TITLE OF INVENTION: No. US20030148943A1el Tachykinin-like Polypeptides and Use There
; FILE REFERENCE: 2680USOP
; CURRENT APPLICATION NUMBER: US/10/168,789A
; CURRENT FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: PCT/JP00/09083
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: JP 11-362638
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: JP 12-066714
; PRIOR FILING DATE: 1999-03-10
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 36
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide
US-10-168-789A-36

Query Match      100.0%; Score 21; DB 14; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FGLM 4
Db      5 FGLM 8

US-10-688-741-2
; Sequence 2, Application US/10688741
; Publication No. US20040106636A1
; GENERAL INFORMATION:
; APPLICANT: Kream, Richard M.
; APPLICANT: Kream, Richard M.
; TITLE OF INVENTION: Method Of Inhibiting Opioid Tolerance Development With Chimeric
; FILE REFERENCE: Kream
; CURRENT APPLICATION NUMBER: US/10/688,741
; CURRENT FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 7
; TYPE: PRT
; ORGANISM: mammalian
US-10-688-741-2

Query Match      100.0%; Score 21; DB 16; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FGLM 4
Db      4 FGLM 7

RESULT 13
US-10-688-741-2
; Sequence 2, Application US/10688741
; Publication No. US20040106636A1
; GENERAL INFORMATION:
; APPLICANT: Kream, Richard M.
; APPLICANT: Kream, Richard M.
; TITLE OF INVENTION: Method Of Inhibiting Opioid Tolerance Development With Chimeric
; FILE REFERENCE: Kream
; CURRENT APPLICATION NUMBER: US/10/688,741
; CURRENT FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 7
; TYPE: PRT
; ORGANISM: mammalian
US-10-688-741-2

Query Match      100.0%; Score 21; DB 16; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FGLM 4
Db      4 FGLM 7

RESULT 14
US-10-168-789A-36
; Sequence 36, Application US/10168789A
; Publication No. US20030148943A1
; GENERAL INFORMATION:
; APPLICANT: ITOH, Yasuaki
; APPLICANT: NISHI, Kazunori
; APPLICANT: KITADA, Chieko
; APPLICANT: INATOMI, No. US20030148943A1uhiro
; TITLE OF INVENTION: No. US20030148943A1el Tachykinin-like Polypeptides and Use There
; FILE REFERENCE: 2680USOP
; CURRENT APPLICATION NUMBER: US/10/168,789A
; CURRENT FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: PCT/JP00/09083
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: JP 11-362638
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: JP 12-066714
; PRIOR FILING DATE: 1999-03-10
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 36
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide
US-10-168-789A-36

Query Match      100.0%; Score 21; DB 14; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FGLM 4
Db      5 FGLM 8
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RESULT 15  
US-10-134-187-1  
; Sequence 1, Application US/10134187  
; Publication No. US20030202981A1  
; GENERAL INFORMATION:  
; APPLICANT: Kream, Richard M.  
; APPLICANT: Kream, Richard M.  
; APPLICANT: Kream, Richard M.  
; TITLE OF INVENTION: Chimeric Hybrid Analgesics  
; FILE REFERENCE: Kream  
; CURRENT APPLICATION NUMBER: US/10/134,187  
; CURRENT FILING DATE: 2002-04-26  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: mammalian  
US-10-134-187-1

Query Match 100.0%; Score 21; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FGLM 4  
Db 6 FGLM 9

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Job time : 128 secs

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OM protein - protein search, using sw model

Run on: August 25, 2004, 14:05:58 ; Search time 32 Seconds  
(without alignments)  
6.453 Million cell updates/sec

Title: US-10-053-669-2  
Perfect score: 21  
Sequence: 1 FGLM 4

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/2/iaa/5A-COMB.pep:\*  
2: /cgn2\_6/ptodata/2/iaa/5B-COMB.pep:\*  
3: /cgn2\_6/ptodata/2/iaa/6A-COMB.pep:\*  
4: /cgn2\_6/ptodata/2/iaa/6B-COMB.pep:\*  
5: /cgn2\_6/ptodata/2/iaa/PCTUS-COMB.pep:\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Length	ID	Description
1	21	100.0	4	1	US-08-441-591-63
2	21	100.0	4	1	US-08-303-362A-63
3	21	100.0	4	4	US-09-265-690C-2
4	21	100.0	4	4	US-09-635-266-3
5	21	100.0	4	4	US-10-230-133-3
6	21	100.0	4	5	PCT-US95-05600-80
7	21	100.0	5	1	US-07-934-553-2
8	21	100.0	5	1	US-08-225-474-2
9	21	100.0	5	2	US-08-070-301-6
10	21	100.0	5	2	US-07-737-371E-6
11	21	100.0	5	2	US-07-737-371E-48
12	21	100.0	5	4	US-09-265-690C-1
13	21	100.0	6	1	US-07-934-553-3
14	21	100.0	6	1	US-08-225-474-3
15	21	100.0	6	1	US-08-430-238-15
16	21	100.0	6	2	US-07-737-371E-5
17	21	100.0	6	3	US-09-317-125-5
18	21	100.0	7	1	US-07-712-828B-7
19	21	100.0	7	2	US-07-737-371E-8
20	21	100.0	8	2	US-07-737-371E-10
21	21	100.0	8	2	US-07-737-371E-56
22	21	100.0	9	1	US-08-346-849-6
23	21	100.0	9	2	US-07-737-371E-60
24	21	100.0	9	2	US-08-293-284A-6
25	21	100.0	9	4	US-08-898-300-6
26	21	100.0	10	1	US-08-088-322-6
27	21	100.0	10	1	US-08-437-820-6

28 21 100.0 10 2 US-07-737-371E-9  
29 21 100.0 10 3 US-09-168-548-2  
30 21 100.0 10 6 5169865-11  
31 21 100.0 11 1 US-07-899-205-1  
32 21 100.0 11 1 US-07-934-553-1  
33 21 100.0 11 1 US-08-184-935-12  
34 21 100.0 11 1 US-08-269-288-2  
35 21 100.0 11 1 US-08-338-484-1  
36 21 100.0 11 1 US-08-175-432-1  
37 21 100.0 11 1 US-08-462-413-2  
38 21 100.0 11 1 US-08-225-474-1  
39 21 100.0 11 1 US-08-391-910-2  
40 21 100.0 11 1 US-08-418-994-2  
41 21 100.0 11 1 US-08-480-505-3  
42 21 100.0 11 1 US-08-391-814-2  
43 21 100.0 11 1 US-08-167-870-1  
44 21 100.0 11 1 US-08-428-488-15  
45 21 100.0 11 1 US-08-255-272-6

## ALIGNMENTS

RESULT 1  
US-08-441-591-63  
; Sequence 63, Application US/08441591  
; Patent No. 5637682  
; GENERAL INFORMATION:  
; APPLICANT: NIEUWLANDT, D., GOLD, L. AND WECKER, M.  
; TITLE OF INVENTION: HIGH-AFFINITY  
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIGANDS  
; TITLE OF INVENTION: TO THE TACHYKININ  
; TITLE OF INVENTION: SUBSTANCE P  
; NUMBER OF SEQUENCES: 66  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: Swanson & Bratschun, L.L.C.  
; STREET: 8400 E. Prentice Avenue, Suite 200  
; CITY: Englewood  
; STATE: Colorado  
; COUNTRY: USA  
; ZIP: 80111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage  
; COMPUTER: IBM compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WordPerfect 5.1  
; CURRENT APPLICATION DATA:  
; FILING DATE: 07/714,131  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/303,362  
; FILING DATE: 9-SEPTEMBER-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/714,131  
; FILING DATE: 10-JUNE-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/931,473  
; FILING DATE: 17-AUGUST-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/117,991  
; FILING DATE: 8-SEPTEMBER 1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/536,428  
; FILING DATE: 11-JUNE-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/964,624  
; FILING DATE: 21-OCTOBER-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Barry J. Swanson  
; REGISTRATION NUMBER: 33,215  
; REFERENCE/DOCKET NUMBER: NEX21/C  
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (303) 793-3333  
; TELEFAX: (303) 793-3433  
; INFORMATION FOR SEQ ID NO: 63:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-441-591-63

Query Match 100.0%; Score 21; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 3e+05; 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4  
Db 1 FGLM 4

RESULT 2  
US-08-303-362A-63  
; Sequence 63, Application US/08303362A  
; Patent No. 5648214  
; GENERAL INFORMATION:  
; APPLICANT: NIEUWLANDT, D., GOLD, L. AND WECKER, M.  
; TITLE OF INVENTION: HIGH-AFFINITY  
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIGANDS  
; TITLE OF INVENTION: TO THE TACHYKININ  
; TITLE OF INVENTION: SUBSTANCE P  
; NUMBER OF SEQUENCES: 66  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Swanson & Bratschun, L.L.C. 200  
; STREET: 8400 E. Prentice Avenue, Suite 200  
; CITY: Englewood  
; STATE: Colorado  
; COUNTRY: USA  
; ZIP: 80111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage  
; COMPUTER: IBM compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WordPerfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/303,362A  
; FILING DATE: 9-SEPTEMBER-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/714,131  
; FILING DATE: 10-JUNE-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/931,473  
; FILING DATE: 17-AUGUST-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/117,991  
; FILING DATE: 8-SEPTEMBER 1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/536,428  
; FILING DATE: 11-JUNE-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/964,624  
; FILING DATE: 21-OCTOBER-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Barry J. Swanson  
; REGISTRATION NUMBER: 33,215  
; REFERENCE/DOCKET NUMBER: NEX21  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (303) 793-3333  
; TELEFAX: (303) 793-3433  
; INFORMATION FOR SEQ ID NO: 63:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4  
; TYPE: amino acid  
; STRANDEDNESS: single

; TOPOLOGY: linear  
; US-08-303-362A-63

Query Match 100.0%; Score 21; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 3e+05; 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4  
Db 1 FGLM 4

RESULT 3  
US-09-265-690C-2  
; Sequence 2, Application US/09265690C  
; Patent No. 6372440  
; GENERAL INFORMATION:  
; APPLICANT: Wells, Ibert  
; TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound Ma  
; TITLE OF INVENTION: for Disease Diagnosis  
; FILE REFERENCE: 1427001  
; CURRENT APPLICATION NUMBER: US/09/265,690C  
; CURRENT FILING DATE: 1999-03-10  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (4)..(4)  
; OTHER INFORMATION: AMIDATION  
; US-09-265-690C-2

Query Match 100.0%; Score 21; DB 4; Length 4;  
Best Local Similarity 100.0%; Pred. No. 3e+05; 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4  
Db 1 FGLM 4

RESULT 4  
US-09-635-266-3  
; Sequence 3, Application US/09635266  
; Patent No. 6455734  
; GENERAL INFORMATION:  
; APPLICANT: Wells, Ibert  
; TITLE OF INVENTION: Antagonists of the magnesium binding defect as therapy agents and  
; TITLE OF INVENTION: methods for treatment of abnormal physiological states  
; FILE REFERENCE: N1427-002  
; CURRENT APPLICATION NUMBER: US/09/635,266  
; CURRENT FILING DATE: 2000-08-09  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 3  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (4)..(4)  
; OTHER INFORMATION: AMIDATION  
; US-09-635-266-3

Query Match 100.0%; Score 21; DB 4; Length 4;  
Best Local Similarity 100.0%; Pred. No. 3e+05; 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4  
Db 1 FGLM 4



Db 1 FGLM 4

RESULT 5

US-10-230-133-3

Sequence 3, Application US/10230133

Patent No. 6664420

GENERAL INFORMATION:

APPLICANT: Wells, Ibert

TITLE OF INVENTION: Antagonists of the magnesium binding defect as therapy agents and methods for treatment of abnormal physiological states

FILE REFERENCE: 2892-106

CURRENT APPLICATION NUMBER: US/10/230,133

CURRENT FILING DATE: 2002-08-29

PRIOR APPLICATION NUMBER: 09/635,266

PRIOR FILING DATE: 2000-08-09

NUMBER OF SEQ ID NOS: 4

SOFTWARE: PatentIn version 3.0

SEQ ID NO 3

LENGTH: 4

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: MOD RES

LOCATION: (4)-(4)

OTHER INFORMATION: AMIDATION

US-10-230-133-3

Query Match 100.0%; Score 21; DB 4; Length 4;

Best Local Similarity 100.0%; Pred. No. 3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4

Db 1 FGLM 4

RESULT 6

PCT-US95-05600-80

Sequence 80, Application PC/TUS9505600

GENERAL INFORMATION:

APPLICANT: GOLD, LARRY

APPLICANT: NIEUMLANDT, DAN

APPLICANT: WECKER, MATTHEW

APPLICANT: SCHNEIDER, DANIEL J.

APPLICANT: FEIGON, JULI

APPLICANT: ALLEN, PATRICK

APPLICANT: SULLENGER, BRUCE A.

APPLICANT: DOUDNA, JENNIFER, A.

TITLE OF INVENTION: HIGH-AFFINITY LIGANDS OF INSULIN RECEPTOR ANTIBODIES, TACHYKININ SUBSTANCE P, HIV INTEGRASE AND HIV-1 REVERSE TRANSCRIPTASE

TITLE OF INVENTION: P, HIV INTEGRASE AND HIV-1 REVERSE TRANSCRIPTASE

NUMBER OF SEQUENCES: 239

CORRESPONDENCE ADDRESS:

ADDRESSEE: Swanson & Bratschun, L.L.C.

STREET: 8400 E. Prentice Avenue, Suite 200

CITY: Englewood

STATE: Colorado

COUNTRY: USA

ZIP: 80111

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MG

MEDIUM TYPE: storage

COMPUTER: IBM compatible

OPERATING SYSTEM: MS-DOS

SOFTWARE: Wordperfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/05600

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

PRIOR APPLICATION NUMBER: 08/238,863

FILING DATE: 06-MAY-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/248,632

FILING DATE: 24-MAY-1994

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/303,362

FILING DATE: 09-SEPTEMBER-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/361,795

FILING DATE: 21-DECEMBER-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/117,991

FILING DATE: 08-SEPTEMBER-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/931,473

FILING DATE: 17-AUGUST-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/964,624

FILING DATE: 21-OCTOBER-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/536,428

FILING DATE: 11-JUNE-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/714,131

FILING DATE: 10-JUNE-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/536,428

FILING DATE: 11-JUNE-1990

ATTORNEY/AGENT INFORMATION:

NAME: Barry J. Swanson

REGISTRATION NUMBER: 33,215

TELECOMMUNICATION INFORMATION:

TELEPHONE: (303) 793-3333

TELEFAX: (303) 793-3433

INFORMATION FOR SEQ ID NO: 80:

SEQUENCE CHARACTERISTICS:

LENGTH: 4 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

PCT-US95-05600-80

Query Match 100.0%; Score 21; DB 5; Length 4;

Best Local Similarity 100.0%; Pred. No. 3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4

Db 1 FGLM 4

RESULT 7

US-07-934-553-2

Sequence 2, Application US/07934553

Patent No. 5314690

GENERAL INFORMATION:

APPLICANT: PATTERSON, ROY

APPLICANT: HARRIS, KATHLEEN E

TITLE OF INVENTION: METHOD AND COMPOSITION FOR REDUCING IGE ANTIBODIES TO SPECIFIC ALLERGENS

TITLE OF INVENTION: ANTIBODIES TO SPECIFIC ALLERGENS

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: TILTON, FALLON, LUNGUMUS & CHESTNUT

STREET: 100 SOUTH WACKER DRIVE

CITY: CHICAGO

STATE: ILLINOIS

COUNTRY: USA

ZIP: 60606-4002

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/934,553  
FILING DATE: 19920821  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/705,071  
FILING DATE: 24-MAY-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: PENTRESS, SUSAN B  
REGISTRATION NUMBER: 31,327  
REFERENCE/DOCKET NUMBER: NU-9033CIP  
TELEPHONE: 312/456-8000  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-07-934-553-2

Query Match 100.0%; Score 21; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 1 FGLM 4  
Db 2 FGLM 5

RESULT 8  
US-08-225-474-2  
Sequence 2, Application US/08225474  
Patent No. 5560915  
GENERAL INFORMATION:  
APPLICANT: Patterson, Roy  
APPLICANT: Harris, Kathleen E.  
TITLE OF INVENTION: Method and Composition for Treating  
TITLE OF INVENTION: Ige Mediated Allergies  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Tilton, Fallon, Lungmus & Chestnut  
STREET: 100 S. Wacker Drive, Suite 960  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606-4002  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/225,474  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/934,553  
FILING DATE: 21-AUG-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/705,071  
FILING DATE: 24-MAY-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Tilton, Timothy L.  
REGISTRATION NUMBER: 16,926  
REFERENCE/DOCKET NUMBER: NU 9033-CIP2  
TELEPHONE: (312)-456-8000  
TELEFAX: (312)-456-7776  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:

LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-225-474-2

Query Match 100.0%; Score 21; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 1 FGLM 4  
Db 2 FGLM 5

RESULT 9  
US-08-070-301-6  
Sequence 6, Application US/08070301  
Patent No. 5871995  
GENERAL INFORMATION:  
APPLICANT: IIDA, Toshio  
APPLICANT: KAMINUMA, Toshihiko  
APPLICANT: FUSE, Yuka  
APPLICANT: TAJIMA, Masahiro  
APPLICANT: YANAGI, Mitsuo  
APPLICANT: OKAMOTO, Hiroshi  
APPLICANT: KISHIMOTO, Jiro  
APPLICANT: IFUKU, Ohji  
APPLICANT: KATO, Ichiro  
TITLE OF INVENTION: ENZYME PARTICIPATING IN C-TERMINAL  
TITLE OF INVENTION: AMIDATION, AND METHOD OF PREPARING SAME AND USE THEREOF  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wegner, Cantor, Mueller & Player, P.C.  
STREET: 1233 20th Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20036-8218  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/070,301  
FILING DATE: 24-MAY-1991  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 1-209687  
FILING DATE: 15-AUG-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 1-181933  
FILING DATE: 31-OCT-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 2-76331  
FILING DATE: 26-MAR-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 2-106412  
FILING DATE: 24-APR-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 2-205475  
FILING DATE: 02-AUG-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Player, William E.  
REGISTRATION NUMBER: 31,409  
REFERENCE/DOCKET NUMBER: P-450-22830  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 887-040  
TELEFAX: (202) 835-0605  
TELEX: 440706  
INFORMATION FOR SEQ ID NO: 6:

## ; SEQUENCE CHARACTERISTICS:

; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-070-301-6

Query Match 100.0%; Score 21; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4  
DB 1 FGLM 4

## RESULT 10

US-07-737-371E-6

; Sequence 6, Application US/07737371E

; Patent No. 5876948

; GENERAL INFORMATION:

; APPLICANT: Yankner, Bruce A.

; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY

; TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)

; NUMBER OF SEQUENCES: 77

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish &amp; Richardson, P.C.

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: MA

; COUNTRY: US

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: Windows95

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/737,371E

; FILING DATE: 29-JUL-1991

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/559,172

; FILING DATE: 27-JUL-1990

; ATTORNEY/AGENT INFORMATION:

; NAME: Freeman, John W.

; REGISTRATION NUMBER: 29,066

; REFERENCE/DOCKET NUMBER: 00108/028002

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-542-5070

; TELEFAX: 617-542-8906

; TELEX: 200154

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 5 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-07-737-371E-6

Query Match 100.0%; Score 21; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4  
DB 2 FGLM 5

## RESULT 11

US-07-737-371E-48

; Sequence 48, Application US/07737371E

; Patent No. 5876948  
; GENERAL INFORMATION:  
; APPLICANT: Yankner, Bruce A.  
; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY  
; TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)  
; NUMBER OF SEQUENCES: 77  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson, P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: US  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows95  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/737,371E  
; FILING DATE: 29-JUL-1991  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/559,172  
; FILING DATE: 27-JUL-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Freeman, John W.  
; REGISTRATION NUMBER: 29,066  
; REFERENCE/DOCKET NUMBER: 00108/028002  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-542-5070  
; TELEFAX: 617-542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 48:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-07-737-371E-48

Query Match 100.0%; Score 21; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4  
DB 2 FGLM 5

## RESULT 12

US-09-265-690C-1

; Sequence 1, Application US/09265690C

; Patent No. 6372440

; GENERAL INFORMATION:

; APPLICANT: Wells, Ibert

; TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound Ma

; TITLE OF INVENTION: for Disease Diagnosis

; FILE REFERENCE: 1427001

; CURRENT APPLICATION NUMBER: US/09/265,690C

; CURRENT FILING DATE: 1999-03-10

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 1

; LENGTH: 5

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: MOD\_RES

; LOCATION: (5)..(5)

; OTHER INFORMATION: AMIDATION

US-09-265-690C-1

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Query Match      100.0%; Score 21; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05; 0; Indels 0;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

Qy      1 FGLM 4
Db      2 FGLM 5

RESULT 13
US-07-934-553-3
; Sequence 3, Application US/07934553
; Patent No. 5314690
; GENERAL INFORMATION:
; APPLICANT: PATTERSON, ROY
; APPLICANT: HARRIS, KATHLEEN E
; TITLE OF INVENTION: METHOD AND COMPOSITION FOR REDUCING Ige
; TITLE OF INVENTION: ANTIBODIES TO SPECIFIC ALLERGENS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TILTON, FALLON, LUNGUMUS & CHESTNUT
; STREET: 100 SOUTH WACKER DRIVE
; CITY: CHICAGO
; STATE: ILLINOIS
; COUNTRY: USA
; ZIP: 60606-4002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 19920821
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/934,553
; FILING DATE: 24-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: FENTRESS, SUSAN B
; REGISTRATION NUMBER: 31,327
; REFERENCE/DOCKET NUMBER: NU-9033CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/456-8000
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-07-934-553-3

Query Match      100.0%; Score 21; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

Qy      1 FGLM 4
Db      3 FGLM 6

RESULT 14
US-08-225-474-3
; Sequence 3, Application US/08225474
; Patent No. 5560915
; GENERAL INFORMATION:
; APPLICANT: Patterson, Roy
; APPLICANT: Harris, Kathleen E.
; TITLE OF INVENTION: Method and Composition for Treating
; TITLE OF INVENTION: Ige Mediated Allergies
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
```

```
; ADDRESSEE: Tilton, Fallon, Lungmus & Chestnut
; STREET: 100 S. Wacker Drive, Suite 960
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-4002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/225,474
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/934,553
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/705,071
; FILING DATE: 24-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Tilton, Timothy L.
; REGISTRATION NUMBER: 16,926
; REFERENCE/DOCKET NUMBER: NU 9033-CIP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)-456-8000
; TELEFAX: (312)-456-7776
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: Peptide
US-08-225-474-3

Query Match      100.0%; Score 21; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

Qy      1 FGLM 4
Db      3 FGLM 6

RESULT 15
US-08-430-238-15
; Sequence 15, Application US/08430238
; Patent No. 5693612
; GENERAL INFORMATION:
; APPLICANT: JONCZYK, ALFRED
; APPLICANT: HOLZEMANN, GUNTER
; APPLICANT: GOODMAN, SIMON
; APPLICANT: KESSLER, HORST
; APPLICANT: HAUSER, ROLAND
; APPLICANT: WERMUTH, JOCHEN
; TITLE OF INVENTION: Cyclopeptides of the Formula I
; NUMBER OF SEQUENCES: 15
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPA)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/430,238
; FILING DATE: 28-APR-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4415310.4
; FILING DATE: 30-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lebovitz, Richard M.
```

; REGISTRATION NUMBER: 37,067  
; REFERENCE/DOCKET NUMBER: MERCK 1692  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 243-6333  
; TELEFAX: (703) 243-6410  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: circular  
; MOLECULE TYPE: peptide  
; HYPOTHEICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: N-terminal  
; US-08-430-238-15

Query Match 100.0%; Score 21; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4  
Db ||||  
3 FGLM 6

Search completed: August 25, 2004, 14:16:53  
Job time : 34 secs

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